

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 8, 2005, 02:10:48 ; Search time 89.0685 Seconds  
(without alignments)  
2104.671 Million cell updates/sec

Title: US-10-627-886-26

Perfect score: 2465

Sequence: 1 MDATTGDTALQAVKQMAT.....GANIAGFTKVDVAKQAGV 476

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1774312 seqs, 393823214 residues

Total number of hits satisfying chosen parameters: 1774312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*  
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22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score  | Query Match % | Length | ID                      | Description       |
|------------|--------|---------------|--------|-------------------------|-------------------|
| 1          | 2465   | 100.0         | 476    | 9 US-09-070-844-26      | Sequence 26, Appl |
| 2          | 2465   | 100.0         | 476    | 16 US-10-627-886-26     | Sequence 26, Appl |
| 3          | 2465   | 100.0         | 487    | 9 US-09-070-844-24      | Sequence 24, Appl |
| 4          | 2465   | 100.0         | 487    | 16 US-10-627-886-24     | Sequence 24, Appl |
| 5          | 2465   | 100.0         | 512    | 9 US-09-070-844-4       | Sequence 4, Appl  |
| 6          | 2465   | 100.0         | 512    | 16 US-10-627-886-4      | Sequence 4, Appl  |
| 7          | 2465   | 100.0         | 526    | 9 US-09-070-844-2       | Sequence 2, Appl  |
| 8          | 2465   | 100.0         | 526    | 16 US-10-627-886-2      | Sequence 2, Appl  |
| 9          | 1309   | 53.1          | 445    | 15 US-10-282-122A-66687 | Sequence 6687, A  |
| 10         | 1300.5 | 52.8          | 444    | 18 US-10-988-943-43     | Sequence 43, Appl |
| 11         | 1297.5 | 52.6          | 444    | 15 US-10-282-122A-65129 | Sequence 65129, A |

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| 14 | 1287.5 | 52.2 | 449 | 15 | US-10-282-122A-67538 | Sequence 67538, A |
| 15 | 1281   | 52.0 | 445 | 15 | US-10-369-493-13947  | Sequence 13947, A |
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| 26 | 1210.5 | 49.0 | 464 | 15 | US-10-369-493-17284  | Sequence 17284, A |
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| 31 | 1201   | 48.7 | 447 | 15 | US-10-282-122A-43284 | Sequence 43284, A |
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| 33 | 1196.5 | 48.5 | 456 | 15 | US-10-425-114-72961  | Sequence 72961, A |
| 34 | 1195.5 | 48.5 | 448 | 15 | US-10-369-493-8215   | Sequence 8215, Ap |
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| 36 | 1191   | 48.3 | 447 | 20 | US-11-073-550-80     | Sequence 80, Appl |
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| 38 | 1185   | 48.1 | 447 | 9  | US-11-073-550-82     | Sequence 82, Appl |
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| 40 | 1182.5 | 48.0 | 448 | 15 | US-10-282-122A-75593 | Sequence 75593, A |
| 41 | 1181   | 47.9 | 447 | 15 | US-10-282-122A-60810 | Sequence 60810, A |
| 42 | 1180.5 | 47.9 | 458 | 15 | US-10-369-493-295    | Sequence 295, App |
| 43 | 1180   | 47.9 | 447 | 15 | US-10-282-122A-72769 | Sequence 72769, A |
| 44 | 1178   | 47.8 | 447 | 15 |                      |                   |
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## ALIGNMENTS

RESULT 1  
US-09-070-844-26  
; Sequence 26, Application US/09070844  
; Patent No. US20020062495A1  
; GENERAL INFORMATION:  
; APPLICANT: Schmidt, Robert R.  
; APPLICANT: Miller, Philip  
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
; TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/070,844  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/725,596  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Whitlock, Ted W.  
; REGISTRATION NUMBER: 36,965  
; REFERENCE/DOCKET NUMBER: UF155

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 476 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-070-844-26

Query Match 100.0%; Score 2465; DB 9; Length 476;  
Best Local Similarity 100.0%; Pred. No. 5.1e-221;  
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 121 GLRFHPSVNLISIMKFLAFQIFKNSLTTLPMGGGKGSDFDPKGSDAEVMRFQCSFMTE 180  
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DB 421 LNWTRVEVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTTKVADAVKAQGAV 476

RESULT 2  
US-10-627-886-26  
Sequence 26, Application US/10627886  
Publication No. US20040128710A1  
GENERAL INFORMATION:  
APPLICANT: Schmidt, Robert R.  
Miller, Philip  
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE  
DEHYDROGENASES AND METHODS OF USE  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESS: Saliwanchik & Saliwanchik  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606-6669  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/627,886

FILING DATE: 24-Jul-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/070,844  
FILING DATE: 01-MAY-98  
APPLICATION NUMBER: 08/725,596  
FILING DATE: 03-OCT-96  
APPLICATION NUMBER: 08/541,033  
FILING DATE: 06-OCT-95  
ATTORNEY/AGENT INFORMATION:  
NAME: Lloyd, Jeff  
REGISTRATION NUMBER: 35,589  
REFERENCE/DOCKET NUMBER: UF-155CD3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (352) 375-8100  
TELEFAX: (352) 372-5800  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 476 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 26:  
US-10-627-886-26

Query Match 100.0%; Score 2465; DB 16; Length 476;  
Best Local Similarity 100.0%; Pred. No. 5.1e-221;  
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKNPVDRQLLTETIFPKDPEQEFMQAVREV 60  
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RESULT 3  
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Sequence 24, Application US/09070844  
Patent No. US20020062495A1  
GENERAL INFORMATION:  
APPLICANT: Schmidt, Robert R.  
Miller, Philip  
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE  
DEHYDROGENASES AND METHODS OF USE  
NUMBER OF SEQUENCES: 26

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Saliwanchik & Saliwanchik  
;; STREET: 2421 N.W. 41st Street, Suite A-1  
;; CITY: Gainesville  
;; STATE: Florida  
;; COUNTRY: USA  
;; ZIP: 32606  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/070,844  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/725,596  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Whitlock, Ted W.  
;; REGISTRATION NUMBER: 36,965  
;; REFERENCE/DOCKET NUMBER: UF155  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (904) 375-8100  
;; TELEFAX: (904) 372-5800  
;; INFORMATION FOR SEQ ID NO: 24:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 487 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-09-070-844-24

Query Match 100.0%; Score 2465; DB 9; Length 487;  
Best Local Similarity 100.0%; Pred. No. 5.3e-221;  
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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DB 12 MDATTGDTALQKAVKQMATKAGTEGLVHGINKPDPVRLQLLTFIMKDPQEQFMOAVREV 71  
  
QY 61 AVSLQPVFEKRPPELLPIFKQIVPEPVRTFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120  
DB 72 AVSLQPVFEKRPPELLPIFKQIVPEPVRTFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 131  
  
QY 121 GLRPHPSVNLSTMKFLAFEQIFKNSLTTLPMGGGKGGSDPDPKGSDAEVMRQCQSFMT 180  
DB 132 GLRPHPSVNLSTMKFLAFEQIFKNSLTTLPMGGGKGGSDPDPKGSDAEVMRQCQSFMT 191  
  
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DB 192 LQRHISYVDVPAGDIGVGAREIGYLFQYKRTIKNTYTGVLTPKQEGYGSSEIRPEATGY 251  
  
QY 241 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLKGAIVLSLSDSQYVYEPNG 300  
DB 252 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLKGAIVLSLSDSQYVYEPNG 311  
  
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DB 312 FTREQLQAVQDMKKKNSARISYKSDTAVYVGDGRRKPWELDCQVDIAFPCCATQNEIDH 371  
  
QY 361 DAELLKHGCOYVVEGANPSTNEATHKNKAGIICPGKAANAGVAVSGLEMTQNRMS 420  
DB 372 DAELLKHGCOYVVEGANPSTNEATHKNKAGIICPGKAANAGVAVSGLEMTQNRMS 431  
  
QY 421 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAGQAV 476  
DB 432 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAGQAV 487

RESULT 4  
US-10-627-886-24

;; Sequence 24, Application US/10627886  
;; Publication No. US20040128710A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Schmidt, Robert R.  
;; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
;; RELATING TO THE .- AND -SUBUNITS OF GLUTAMATE  
;; DEHYDROGENASES AND METHODS OF USE  
;;  
;; NUMBER OF SEQUENCES: 26  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Saliwanchik & Saliwanchik  
;; STREET: 2421 N.W. 41st Street, Suite A-1  
;; CITY: Gainesville  
;; STATE: Florida  
;; COUNTRY: USA  
;; ZIP: 32606-6669  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/10/627,886  
;; FILING DATE: 24-Jul-2003  
;; CLASSIFICATION: <Unknown>  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 09/070,844  
;; FILING DATE: 01-MAY-98  
;; APPLICATION NUMBER: 08/725,596  
;; FILING DATE: 03-OCT-96  
;; APPLICATION NUMBER: 08/541,033  
;; FILING DATE: 06-OCT-95  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Lloyd, Jeff  
;; REGISTRATION NUMBER: 35,589  
;; REFERENCE/DOCKET NUMBER: UP-155CD3  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (352) 375-8100  
;; TELEFAX: (352) 372-5800  
;; INFORMATION FOR SEQ ID NO: 24:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 487 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 24:  
;; US-10-627-886-24  
  
Query Match 100.0%; Score 2465; DB 16; Length 487;  
Best Local Similarity 100.0%; Pred. No. 5.3e-221;  
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKPDPVRLQLLTFIMKDPQEQFMOAVREV 60  
DB 12 MDATTGDTALQKAVKQMATKAGTEGLVHGINKPDPVRLQLLTFIMKDPQEQFMOAVREV 71  
  
QY 61 AVSLQPVFEKRPPELLPIFKQIVPEPVRTFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120  
DB 72 AVSLQPVFEKRPPELLPIFKQIVPEPVRTFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 131  
  
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DB 132 GLRPHPSVNLSTMKFLAFEQIFKNSLTTLPMGGGKGGSDPDPKGSDAEVMRQCQSFMT 191  
  
QY 181 LQRHISYVDVPAGDIGVGAREIGYLFQYKRTIKNTYTGVLTPKQEGYGSSEIRPEATGY 240  
DB 192 LQRHISYVDVPAGDIGVGAREIGYLFQYKRTIKNTYTGVLTPKQEGYGSSEIRPEATGY 251  
  
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DB 252 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLKGAIVLSLSDSQYVYEPNG 311  
  
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Db 312 FTREQQAQVDMKKKNSARISEYKSDTAVYVGGDRKPEWELDCQVDIAFPCCATQNEIDEH 371
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QY 421 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGA 476
Db 432 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGA 487

RESULT 5
US-09-070-844-4
; Sequence 4, Application US/09070844
; Patent No. US20020062495A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,844
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,596
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UF155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 512 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-070-844-4

Query Match 100.0%; Score 2465; DB 9; Length 512;
Best Local Similarity 100.0%; Pred. No. 5.7e-221;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDATTGDTALQAKVQKATKAGTEGLVHGINKPNPVRQLLTIFPMKDPEQBFMQAVREV 60
Db 37 MDATTGDTALQAKVQKATKAGTEGLVHGINKPNPVRQLLTIFPMKDPEQBFMQAVREV 96
QY 61 AVSLQVPEKRPPELLPIFKQIVPEPRVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
Db 97 AVSLQVPEKRPPELLPIFKQIVPEPRVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 156
QY 121 GLRFPSPVNLIMKFLAPFQIFKNSLTTLPMGGGKGSGDFDPKSKSDAEVMEFCQSPFMT 180
Db 157 GLRFPSPVNLIMKFLAPFQIFKNSLTTLPMGGGKGSGDFDPKSKSDAEVMEFCQSPFMT 216
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QY 181 LQRHISYVDVPAGDIGVGAREIGYLFQGYKRITKNYTGVLTPKGOEYGSSEIRPEATGY 240
Db 217 LQRHISYVDVPAGDIGVGAREIGYLFQGYKRITKNYTGVLTPKGOEYGSSEIRPEATGY 276
QY 241 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLKGAIVLSLSDSQGYVYEPNG 300
Db 277 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLKGAIVLSLSDSQGYVYEPNG 336
QY 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGGDRKPEWELDCQVDIAFPCCATQNEIDEH 360
Db 337 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGGDRKPEWELDCQVDIAFPCCATQNEIDEH 396
QY 361 DAELLIKHGCQVVEGANPSTNEAIHKYNKAGIIPCCKAANAGGAVVSGLEMTQNRMS 420
Db 397 DAELLIKHGCQVVEGANPSTNEAIHKYNKAGIIPCCKAANAGGAVVSGLEMTQNRMS 456
QY 421 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGA 476
Db 457 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGA 512

RESULT 6
US-10-627-886-4
; Sequence 4, Application US/10627886
; Publication No. US20040128710A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606-6669
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/627,886
; FILING DATE: 24-Jul-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/070,844
; FILING DATE: 01-MAY-98
; APPLICATION NUMBER: 08/725,596
; FILING DATE: 03-OCT-96
; APPLICATION NUMBER: 08/541,033
; FILING DATE: 06-OCT-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Lloyd, Jeff
; REGISTRATION NUMBER: 35,589
; REFERENCE/DOCKET NUMBER: UF-155CD3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 512 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-627-886-4

Query Match 100.0%; Score 2465; DB 16; Length 512;
Best Local Similarity 100.0%; Pred. No. 5.7e-221;
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Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKPDPVRLQLTEIFMKDPEQBFMQAVREV 60  
DB 37 MDATTGDTALQKAVKQMATKAGTEGLVHGINKPDPVRLQLTEIFMKDPEQBFMQAVREV 96  
QY 61 AVSLQPVFEKPELLPIFKQIVPEPVRVITFRVSWLDDAGNLQVNRGRFRVQYSSAIGPYKG 120  
DB 97 AVSLQPVFEKPELLPIFKQIVPEPVRVITFRVSWLDDAGNLQVNRGRFRVQYSSAIGPYKG 156  
QY 121 GLRFHPSVNLKIMKFLAFEQIFKNSLTTLPMGGGKGGSDPDPKGSKDAEVMRFCOSFMTE 180  
DB 157 GLRFHPSVNLKIMKFLAFEQIFKNSLTTLPMGGGKGGSDPDPKGSKDAEVMRFCOSFMTE 216  
QY 181 LQRHISYVDVPAGDIGVAREIGYLFQGYKRITKNTYTGVLTPKGQYGGSEIRPEATGY 240  
DB 217 LQRHISYVDVPAGDIGVAREIGYLFQGYKRITKNTYTGVLTPKGQYGGSEIRPEATGY 276  
QY 241 GAVLFVENVLKDKGESLKGKRCCLVSGAGNVAQYCAELLLLEKGAIVLSLSDSQGYVYEPNG 300  
DB 277 GAVLFVENVLKDKGESLKGKRCCLVSGAGNVAQYCAELLLLEKGAIVLSLSDSQGYVYEPNG 336  
QY 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCCATQNEIDEH 360  
DB 337 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCCATQNEIDEH 396  
QY 361 DAELLIKHGCGQYVEGANMPSTNEAIHKYNKAGIIPCCKAANAGGAVVSGLEMTQNRMS 420  
DB 397 DAELLIKHGCGQYVEGANMPSTNEAIHKYNKAGIIPCCKAANAGGAVVSGLEMTQNRMS 456  
QY 421 LNWTRREEVRDKLERIMKDIYDSAMGPSRRYNDVLAAGANIAGFTKVADAVKAQGAV 476  
DB 457 LNWTRREEVRDKLERIMKDIYDSAMGPSRRYNDVLAAGANIAGFTKVADAVKAQGAV 512

RESULT 7

US-09-070-844-2  
; Sequence 2, Application US/09070844  
; Patent No. US20020062495A1  
; GENERAL INFORMATION:  
; APPLICANT: Schmidt, Robert R.  
; APPLICANT: Miller, Philip  
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
; RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE  
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/070,844  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/725,596  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Whitlock, Ted W.  
; REGISTRATION NUMBER: 36,965  
; REFERENCE/DOCKET NUMBER: UP155  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (904) 375-8100  
; TELEFAX: (904) 372-5800  
; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 526 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-070-844-2

Query Match 100.0%; Score 2465; DB 9; Length 526;  
Best Local Similarity 100.0%; Pred. No. 5.9e-221;  
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKPDPVRLQLTEIFMKDPEQBFMQAVREV 60  
DB 51 MDATTGDTALQKAVKQMATKAGTEGLVHGINKPDPVRLQLTEIFMKDPEQBFMQAVREV 110  
QY 61 AVSLQPVFEKPELLPIFKQIVPEPVRVITFRVSWLDDAGNLQVNRGRFRVQYSSAIGPYKG 120  
DB 111 AVSLQPVFEKPELLPIFKQIVPEPVRVITFRVSWLDDAGNLQVNRGRFRVQYSSAIGPYKG 170  
QY 121 GLRFHPSVNLKIMKFLAFEQIFKNSLTTLPMGGGKGGSDPDPKGSKDAEVMRFCOSFMTE 180  
DB 171 GLRFHPSVNLKIMKFLAFEQIFKNSLTTLPMGGGKGGSDPDPKGSKDAEVMRFCOSFMTE 230  
QY 181 LQRHISYVDVPAGDIGVAREIGYLFQGYKRITKNTYTGVLTPKGQYGGSEIRPEATGY 240  
DB 231 LQRHISYVDVPAGDIGVAREIGYLFQGYKRITKNTYTGVLTPKGQYGGSEIRPEATGY 290  
QY 241 GAVLFVENVLKDKGESLKGKRCCLVSGAGNVAQYCAELLLLEKGAIVLSLSDSQGYVYEPNG 300  
DB 281 GAVLFVENVLKDKGESLKGKRCCLVSGAGNVAQYCAELLLLEKGAIVLSLSDSQGYVYEPNG 350  
QY 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCCATQNEIDEH 360  
DB 351 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCCATQNEIDEH 410  
QY 361 DAELLIKHGCGQYVEGANMPSTNEAIHKYNKAGIIPCCKAANAGGAVVSGLEMTQNRMS 420  
DB 411 DAELLIKHGCGQYVEGANMPSTNEAIHKYNKAGIIPCCKAANAGGAVVSGLEMTQNRMS 470  
QY 421 LNWTRREEVRDKLERIMKDIYDSAMGPSRRYNDVLAAGANIAGFTKVADAVKAQGAV 476  
DB 471 LNWTRREEVRDKLERIMKDIYDSAMGPSRRYNDVLAAGANIAGFTKVADAVKAQGAV 526

RESULT 8

US-10-627-886-2  
; Sequence 2, Application US/10627886  
; Publication No. US20040128710A1  
; GENERAL INFORMATION:  
; APPLICANT: Schmidt, Robert R.  
; APPLICANT: Miller, Philip  
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
; RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE  
; DEHYDROGENASES AND METHODS OF USE  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606-6669  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/627,886  
; FILING DATE: 24-Jul-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/070,844

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/ FILING DATE: 01-MAY-98
/ APPLICATION NUMBER: 08/725,596
/ FILING DATE: 03-OCT-96
/ APPLICATION NUMBER: 08/541,033
/ FILING DATE: 06-OCT-95
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lloyd, Jeff
/ REGISTRATION NUMBER: 35,589
/ REFERENCE/DOCKET NUMBER: UP-155CD3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (352) 375-8100
/ TELEFAX: (352) 372-5800
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 526 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-627-886-2

Query Match      100.0%; Score 2465; DB 16; Length 526;
Best Local Similarity 100.0%; Pred. No. 5.9e-221;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDATTGDTALQKAVKQKATKAGTEGLVHGIIKNDPVRQLLTIFPKDPEQEFMQAVREV 60
Db MDATTGDTALQKAVKQKATKAGTEGLVHGIIKNDPVRQLLTIFPKDPEQEFMQAVREV 110

QY 61 AVSLQPVFKRPPELLPIFQIIVEPVRVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
Db AVSLQPVFKRPPELLPIFQIIVEPVRVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 170

QY 121 GLRPHSPVNLSTIMKFLAPFQIPKNSLTTLPMGGGKGSDFDPKGSKDAEVMRFGCSPMTE 180
Db GLRPHSPVNLSTIMKFLAPFQIPKNSLTTLPMGGGKGSDFDPKGSKDAEVMRFGCSPMTE 230

QY 181 LQRHSYVQDVDPAGDIGVCAREIGYLFQYKAITKNYTGVLTPKQEGYGSIRPEATGY 240
Db LQRHSYVQDVDPAGDIGVCAREIGYLFQYKAITKNYTGVLTPKQEGYGSIRPEATGY 290

QY 241 GAVLFVENVLKDGBESLKGKRLCVSGAGNVAQYCAELLLEKGAIVLSLSDSGYVYEPNG 300
Db GAVLFVENVLKDGBESLKGKRLCVSGAGNVAQYCAELLLEKGAIVLSLSDSGYVYEPNG 350

QY 301 FTREQLQAVQDMKKKNNNSARISEYKSDTAVYVGDRRKRWELDCQVDIAPPQATQNEIDEH 360
Db FTREQLQAVQDMKKKNNNSARISEYKSDTAVYVGDRRKRWELDCQVDIAPPQATQNEIDEH 410

QY 361 DAELLIKHGCQVYVVGANMPSTNEAIHKYNKAGIICPCGAANAGGVAUSGLEMTQNRMS 420
Db DAELLIKHGCQVYVVGANMPSTNEAIHKYNKAGIICPCGAANAGGVAUSGLEMTQNRMS 470

QY 421 LNWTRREEVRDKLERIMKDIYDSAMGPSRRYNYVDLAAGANIAGFTTKVADAVKAQGV 476
Db LNWTRREEVRDKLERIMKDIYDSAMGPSRRYNYVDLAAGANIAGFTTKVADAVKAQGV 526

RESULT 9
US-10-282-122A-66687
/ Sequence 66687, Application US/10282122A
/ Publication No. US20040029129A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Lianguo
/ APPLICANT: Zamudio, Carlos
/ APPLICANT: Malone, Cheryl
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Kari
/ APPLICANT: Zyskind, Judith
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John
/ APPLICANT: Carr, Grant
/ APPLICANT: Yamamoto, Robert

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/ APPLICANT: Forsyth, R.
/ APPLICANT: Xu, H.
/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
/ FILE REFERENCE: ELITRA.034A
/ CURRENT APPLICATION NUMBER: US/10/282,122A
/ CURRENT FILING DATE: 2003-02-20
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/230,335
/ PRIOR FILING DATE: 2000-09-06
/ PRIOR APPLICATION NUMBER: 60/230,347
/ PRIOR FILING DATE: 2000-09-09
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/267,636
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 78614
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 66687
/ LENGTH: 445
/ TYPE: PRT
/ ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-66687

Query Match      53.1%; Score 1309; DB 15; Length 445;
Best Local Similarity 59.2%; Pred. No. 4.5e-113;
Matches 263; Conservative 55; Mismatches 120; Indels 6; Gaps 4;

QY 36 VQLLTETFMKDPQEQEFMQAVREVAVSLQPVFKRPPELLP--IFKQIVEPVRVITPRVS 93
Db VDAFLERLKRDPQEQEFMQAVEEVLRSWLPFLEANPHYLEAGIIRIVEPERAILFRVP 64

QY 94 WLDAGNLQVNRGFRVQYSSAIGPYKGLRPHSPVNLSTIMKFLAPFQIPKNSLTTLPMGG 153
Db WDDQGRVVRNRGFRVQYSSAIGPYKGLRPHSPVNLSTIMKFLAPFQIPKNSLTTLPMGG 124

QY 154 KGGSDDPDKGSKDAEVMRFGCSPMTELQRIHSYVQDVDPAGDIGVGAREIGYLFQYKRI 213
Db KGGSDDPDKGSKDAEVMRFGCSPMTELYRHVGADLDVDPAGDIGVGAREIGYLFQYKRI 184

QY 214 TKNYTGVLTPKQEGYGSIRPEATGYGAVLFVENVLKDGBESLKGKRLCVSGAGNVAQY 273
Db SNQFTSVLTGKLSYGGSLIRPEATGFCGVYFAQEMLKDGRGPDGQGVVAISGSGNVAQY 244

QY 274 CAELLLEKGAIVLSLSDSGYVYEPNGFTREQLQAVQDMKKKNNNSARISEYKSDTAVYV 333
Db AARKVMEGGKVIISLSDSSEGLTYABAGLSDSQWELMELKNVRR--GRIREMABQFSLOQL 303

QY 334 DRRKRWELDCQVDIAPPQATQNEIDEHDAELLIKHGCQVYVVGANMPSTNEAIHKYNKAG 393
Db EGRFPWGLAC--DIALPCATQNEIDAEADARLLANGCVCAEGANMSTLEAVDLFLBAG 361

QY 394 IICYCPGAANAGGVAUSGLEMTQNRMSLNWTRREEVRDKLERIMKDIYDSA-MGPSRRYV 452
Db ILYAPGKASNAGGVAUSGLEMSQNMRLRWSEGEVDTKLHGIMQSIHHAICLLYGEQGRV 421

QY 453 DLAAGANIAGFTTKVADAVKAQGV 476
Db NYVKGANIAGFTVKVADAMLAQGV 445

RESULT 10

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US-10-988-943-43
; Sequence 43, Application US/10988943
; Publication No. US20050176085A1
; GENERAL INFORMATION:
; APPLICANT: Center for Genetic Engineering and Biotechnology
; TITLE OF INVENTION: METHOD OF SELECTIVE PEPTIDE ISOLATION FOR THE
; TITLE OF INVENTION: IDENTIFICATION AND QUANTITATIVE ANALYSIS OF PROTEINS IN
; TITLE OF INVENTION: COMPLEX MIXTURES.
; FILE REFERENCE: Proteomics CU2003-269
; CURRENT APPLICATION NUMBER: US/10/988,943
; CURRENT FILING DATE: 2004-11-15
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Neisseria meningitidis (group B)
US-10-988-943-43

Query Match      52.8%; Score 1300.5; DB 18; Length 444;
Best Local Similarity 57.4%; Pred. No. 2.8e-112;
Matches 257; Conservative 72; Mismatches 104; Indels 15; Gaps 6;

QY 35 DVRQLLTETFMKDPQEQEFMQAVREAVSLQPVFKRPPELL--PIFKQIVPEPVITFRV 92
Db 3 DLNLTFLANLKQRPNQEPFHQAVEEVFMSLDPPFLAKNPKYTOQSLLERIVEPVRV 62
QY 93 SWLDDAGNLQVNRGRFRVQYSSAIGPYKGLRPHPSVNLISIMKFLAEPQIFKNSLTPLMG 152
Db 63 TWQDDKGQVQVNRGRVQVMSAIGPYKGLRPHPTVDLGLVKFLAEPQVFNALTTPLMG 122
QY 153 GKGGSDFDPKGSKDAEVMRFQCSFMTLQRHISYVQDVPAGDIGVGAREIGYLFQYKR 212
Db 123 GKGGSDFDPKGSKDAEVMRFQCSFMTLQRHISYVQDVPAGDIGVGAREIGYLFQYKR 182
QY 213 ITKNYTGVLTPKQEGYGGSEIRPEATGYGAVLFVENVLKDGESLKGKRCVSGAGNVAQ 272
Db 183 IRNEFTSVLTGKLEWGGSLIRPEATGYGCVYFAQAMLTQNRNDSFEGKRVLSGSGNVAQ 242
QY 273 YCAELLEKGAIIVLSLSDSQGYVVEP-NGFTREQLQAVQDMKKNSARISYKSDTAVY 331
Db 243 YAAEKAIQLGAKVLTVDSDGFLPFDIGMTAEQAALLIELKEVRE-RVATYAKEQGLQ 301
QY 332 VDRRKPEWELDCQVDIAFPQATONEIDHDAELLIRKHGCGQYVVEGANMPSTNEAIHKYNK 391
Db 302 YFEKQKPMGV--AAEIALPCATQNELDEEAATLLANGCVYVAEGANMSTLGAVEQFTK 359
QY 392 AGIIPCCKAANAGGAVVSGLEWNTQNRMSLNTWREVRDKLERIMKDIYDSAMGPSRRY- 450
Db 360 AGILYAPGRASNAGGAVTSGLMSQNAIRLSWTREVRDQLRFGIMQSIHESCL----KYG 415
QY 451 ----NVDLAAGANIAGFTKVADAVKAQG 474
Db 416 KVGDTVYVNGANIAGFVKVADAMLAQG 443

RESULT 11
US-10-282-122A-65129
; Sequence 65129, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangou
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65129
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-282-122A-65129

Query Match      52.6%; Score 1297.5; DB 15; Length 444;
Best Local Similarity 57.4%; Pred. No. 5.4e-112;
Matches 257; Conservative 70; Mismatches 106; Indels 15; Gaps 6;

QY 35 DVRQLLTETFMKDPQEQEFMQAVREAVSLQPVFKRPPELL--PIFKQIVPEPVITFRV 92
Db 3 DLNLTFLANLKQRPNQEPFHQAVEEVFMSLDPPFLAKNPKYTOQSLLERIVEPVRV 62
QY 93 SWLDDAGNLQVNRGRFRVQYSSAIGPYKGLRPHPSVNLISIMKFLAEPQIFKNSLTPLMG 152
Db 63 TWQDDKGQVQVNRGRVQVMSAIGPYKGLRPHPTVDLGLVKFLAEPQVFNALTTPLMG 122
QY 153 GKGGSDFDPKGSKDAEVMRFQCSFMTLQRHISYVQDVPAGDIGVGAREIGYLFQYKR 212
Db 123 GKGGSDFDPKGSKDAEVMRFQCSFMTLQRHISYVQDVPAGDIGVGAREIGYLFQYKR 182
QY 213 ITKNYTGVLTPKQEGYGGSEIRPEATGYGAVLFVENVLKDGESLKGKRCVSGAGNVAQ 272
Db 183 IRNEFTSVLTGKLEWGGSLIRPEATGYGCVYFAQAMLTQNRNDSFEGKRVLSGSGNVAQ 242
QY 273 YCAELLEKGAIIVLSLSDSQGYVVEP-NGFTREQLQAVQDMKKNSARISYKSDTAVY 331
Db 243 YAAEKAIQLGAKVLTVDSDGFLPFDIGMTAEQAALLIELKEVRE-RVATYAKEQGLQ 301
QY 332 VDRRKPEWELDCQVDIAFPQATONEIDHDAELLIRKHGCGQYVVEGANMPSTNEAIHKYNK 391
Db 302 YFEKQKPMGV--AAEIALPCATQNELDEEAATLLANGCVYVAEGANMSTLGAVEQFTK 359
QY 392 AGIIPCCKAANAGGAVVSGLEWNTQNRMSLNTWREVRDKLERIMKDIYDSAMGPSRRY- 450
Db 360 AGILYAPGRASNAGGAVTSGLMSQNAIRLSWTREVRDQLRFGIMQSIHESCL----KYG 415
QY 451 ----NVDLAAGANIAGFTKVADAVKAQG 474
Db 416 KVGDTVYVNGANIAGFVKVADAMLAQG 443

RESULT 12
US-10-282-122A-66041
; Sequence 66041, Application US/10282122A
```

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/ Publication No. US20040029129A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Liangsu
/ APPLICANT: Zamudio, Carlos
/ APPLICANT: Malone, Cheryl
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Kari
/ APPLICANT: Zyskind, Judith
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John
/ APPLICANT: Carr, Grant
/ APPLICANT: Yamamoto, Robert
/ APPLICANT: Forsyth, R.
/ APPLICANT: Xu, H.
/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
/ FILE REFERENCE: ELITRA.034A
/ CURRENT APPLICATION NUMBER: US/10/282,122A
/ CURRENT FILING DATE: 2003-02-20
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/230,335
/ PRIOR FILING DATE: 2000-09-06
/ PRIOR APPLICATION NUMBER: 60/230,347
/ PRIOR FILING DATE: 2000-09-09
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/267,636
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 78614
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 66041
/ LENGTH: 444
/ TYPE: PRT
/ ORGANISM: Neisseria meningitidis
/ US-10-282-122A-66041

Query Match          52.5%; Score 1294.5; DB 15; Length 444;
Best Local Similarity 57.1%; Pred. No. 1e-111;
Matches 256; Conservative 72; Mismatches 105; Indels 15; Gaps 6;

QY 35 DVROLLTEIFMKDPQEQEFMQAVREAVSLQPVFEKRPPELL--PIFKQIVPEPRTVTRV 92
Db 3 DLNTLFLANLKQRPNPQEPHQAQVEVFMSLDPLFLAKNPKYTQOSLLERIVPEPRTVTRV 62
QY 93 SWLDDAGNLQVNRGRVQYSSAIGPYKGLRPHSPVNLINMKELAFEQIPKNSLTTLPMG 152
Db 63 TWQDDKGVQVNRGRVQYSSAIGPYKGLRPHSPVNLINMKELAFEQIPKNSLTTLPMG 122
QY 153 GKGGSDFDPKGSDAEVMRFQCSFMTLORHISVVDVPAGDIGVGAREIGYLFQGYKR 212
Db 123 GKGGSDFDPKGSDAEVMRFQCSFMTLORHISVVDVPAGDIGVGAREIGYLFQGYKR 182
QY 213 ITKNYTVGLTPKQYGGSEIRPEATGYGAVLFVENVLKDKGSLKGRCLVSGAGNVAQ 272
Db 183 IRNEFFSVLTGKLEWGGSLIRPEATGYGCVYFAQAMLQTRNDSFEGKRVLISGSGNVAQ 242
QY 273 YCAELLLEKGAIVLSLSDSQYVYEP-NGFTREQLQAVQDMKKNSARISEYKSDTAVY 331
Db 243 YAAEKAQLGAKVLTVDSDNSGVFLFDSGMSQAALAEIUEKVRRE-RVATYAKEQGLQ 301
QY 332 VGDRRKPWELDCQVDIAFPCCATQNEIDEHDAELLIKHGCGQYVVEGANMPSTNEAIHKYNK 391
Db 302 YFENQKPGV--AAEIALPCATQNELDEAAKTLANGCYVVAEGANMPSTGLGAVEQFIK 359
QY 392 AGIYCPGKAANAGGAVSGLQEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRY- 450
Db 360 AGIYAPGKASNAGGAVSGLQEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRY- 450
QY 451 ----NVDLAAGANTAGTCKVADAVKAQ 474
Db 416 KVGDTVNYVNGANTAGTCKVADAVKAQ 443

RESULT 13
US-10-275-026A-152
/ Sequence 152, Application US/10275026A
/ Publication No. US2004008770A1
/ GENERAL INFORMATION:
/ APPLICANT: Tang, Christoph
/ TITLE OF INVENTION: Virulence Genes, Proteins, and Their Use
/ FILE REFERENCE: GJB-6436
/ CURRENT APPLICATION NUMBER: US/10/275,026A
/ CURRENT FILING DATE: 2003-10-31
/ PRIOR APPLICATION NUMBER: PCT/GB01/02003
/ PRIOR FILING DATE: 2001-05-08
/ PRIOR APPLICATION NUMBER: GB 0011108.8
/ PRIOR FILING DATE: 2000-05-08
/ NUMBER OF SEQ ID NOS: 214
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 152
/ LENGTH: 444
/ TYPE: PRT
/ ORGANISM: Neisseria meningitidis
/ US-10-275-026A-152

Query Match          52.5%; Score 1294.5; DB 15; Length 444;
Best Local Similarity 57.1%; Pred. No. 1e-111;
Matches 256; Conservative 72; Mismatches 105; Indels 15; Gaps 6;

QY 35 DVROLLTEIFMKDPQEQEFMQAVREAVSLQPVFEKRPPELL--PIFKQIVPEPRTVTRV 92
Db 3 DLNTLFLANLKQRPNPQEPHQAQVEVFMSLDPLFLAKNPKYTQOSLLERIVPEPRTVTRV 62
QY 93 SWLDDAGNLQVNRGRVQYSSAIGPYKGLRPHSPVNLINMKELAFEQIPKNSLTTLPMG 152
Db 63 TWQDDKGVQVNRGRVQYSSAIGPYKGLRPHSPVNLINMKELAFEQIPKNSLTTLPMG 122
QY 153 GKGGSDFDPKGSDAEVMRFQCSFMTLORHISVVDVPAGDIGVGAREIGYLFQGYKR 212
Db 123 GKGGSDFDPKGSDAEVMRFQCSFMTLORHISVVDVPAGDIGVGAREIGYLFQGYKR 182
QY 213 ITKNYTVGLTPKQYGGSEIRPEATGYGAVLFVENVLKDKGSLKGRCLVSGAGNVAQ 272
Db 183 IRNEFFSVLTGKLEWGGSLIRPEATGYGCVYFAQAMLQTRNDSFEGKRVLISGSGNVAQ 242
QY 273 YCAELLLEKGAIVLSLSDSQYVYEP-NGFTREQLQAVQDMKKNSARISEYKSDTAVY 331
Db 243 YAAEKAQLGAKVLTVDSDNSGVFLFDSGMSQAALAEIUEKVRRE-RVATYAKEQGLQ 301
QY 332 VGDRRKPWELDCQVDIAFPCCATQNEIDEHDAELLIKHGCGQYVVEGANMPSTNEAIHKYNK 391
Db 302 YFENQKPGV--AAEIALPCATQNELDEAAKTLANGCYVVAEGANMPSTGLGAVEQFIK 359
QY 392 AGIYCPGKAANAGGAVSGLQEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRY- 450
Db 360 AGIYAPGKASNAGGAVSGLQEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRY- 450
QY 451 ----NVDLAAGANTAGTCKVADAVKAQ 474
Db 416 KVGDTVNYVNGANTAGTCKVADAVKAQ 443

RESULT 14
US-10-282-122A-67538
/ Sequence 67538, Application US/10282122A
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Publication No. US20040029129A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Lianguu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Haeelbeck, Robert  
APPLICANT: Ohlsen, Kari  
APPLICANT: Zyskind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.  
APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A  
CURRENT APPLICATION NUMBER: US/10/282,122A  
CURRENT FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/230,335  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/230,347  
PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/267,636  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 67538  
LENGTH: 449  
TYPE: PRT  
ORGANISM: Pseudomonas putida  
US-10-282-122A-67538

Query Match 52.2%; Score 1287.5; DB 15; Length 449;  
Best Local Similarity 58.2%; Pred. No. 4.7e-111;  
Matches 259; Conservative 55; Mismatches 124; Indels 7; Gaps 4;  
QY 36 VRQLLTFMKDPEQOEQAVREAVAVSLQVFEKRPPELLP--IFKQIVEPERVITFRVS 93  
DB 8 VDNFLARLQKRDGDPQEPHQAVEEVLRTLWPLEANPHYLSGILRVMVEPERAVLFRVS 67  
QY 94 WLDDAGNLQVNRGFRVQYSSAIGPYKGLRPHSPVNLTKFLAEPQIFKNSLTLPMSG 153  
DB 68 WDDQGVQVNRGFRVQYSSAIGPYKGLRPHSPVNLTKFLAEPQIFKNSLTLPMSG 127  
QY 154 KGSGSDFDPKGSDAEVMRFCQSFMTLQRIHSYVDVPAGDIGVGAREIGYLFQYKRI 213  
DB 128 KGSGSDFDPKGSDAEVMRFCQSFMTLQRIHSYVDVPAGDIGVGAREIGYLFQYKRI 187  
QY 214 TKNTYGVLTTPKGQYGGSEIRPEATGYGAVLFVENVLKDGESLKGKCLVSGAGNVAQY 273  
DB 188 ANQFTSVLTGKMTYGGSLIRPEATGYGCVYFAEEMLRQDKRIDRGRVAVSGGNVAQY 247  
QY 274 CAELLEKGAIVLSLSDSGYVVEPNFTREQLQAVQDMKKNSARISEYKSDTAVVVG 333  
DB 248 AARKVMDLGGKVISLSDEGTYAAGLTDAQWDALMELKNVKR-GRISELAGQGLEFR 306  
QY 334 DRKPKWELDCQVDIAFPQCATQNEIDEHDAELLIKHGCOYVVEGANMPSTNEAIHKYNKAG 393

DB 307 KGQTPWSLPC--DIALPCATQNELGAEDARTLLRNGCI CVAEGANMPTTLEAVDIFLDAG 364  
QY 394 ILYCPGKAANAGGAVVSGLEMTQNRMSLNTWTRREEVDRDKLERIMKDIYDSAM--GPSRRYV 451  
DB 365 ILYAFGKASNAGGAVVSGLEMSQNRMLLWTAGVDSKLNIMQSIHACHVHYGEADOR 424  
QY 452 VDLAAGANIAGFTKVDADVAKQAGV 476  
DB 425 INYVKGANIAGFVKVADAMLAQGVV 449

## RESULT 15

US-10-369-493-13947  
Sequence 13947, Application US/10369493  
Publication No. US20030233675A1  
GENERAL INFORMATION:  
APPLICANT: Cao, Yongwei  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Slater, Steven C.  
APPLICANT: Goldman, Barry S.  
APPLICANT: Chen, Xianfeng  
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
FILE REFERENCE: 38-10(52052)B  
CURRENT APPLICATION NUMBER: US/10/369,493  
CURRENT FILING DATE: 2003-02-28  
PRIOR APPLICATION NUMBER: US 60/360,039  
PRIOR FILING DATE: 2002-02-21  
NUMBER OF SEQ ID NOS: 47374  
SEQ ID NO 13947  
LENGTH: 445  
TYPE: PRT  
ORGANISM: Pseudomonas fluorescens  
US-10-369-493-13947

Query Match 52.0%; Score 1281; DB 15; Length 445;  
Best Local Similarity 58.1%; Pred. No. 1.9e-110;  
Matches 258; Conservative 59; Mismatches 121; Indels 6; Gaps 4;

QY 36 VRQLLTFMKDPEQOEQAVREAVAVSLQVFEKRPPELLP--IFKQIVEPERVITFRVS 93  
DB 5 VESFLARLKKRDPDQEPHQAVEEVLRLSLWPLEANPHYLTSGILRICEPERAVVFRVS 64  
QY 94 WLDDAGNLQVNRGFRVQYSSAIGPYKGLRPHSPVNLTKFLAEPQIFKNSLTLPMSG 153  
DB 65 WDDQGVQVNRGFRVQYSSAIGPYKGLRPHSPVNLTKFLAEPQIFKNSLTLPMSG 124  
QY 154 KGSGSDFDPKGSDAEVMRFCQSFMTLQRIHSYVDVPAGDIGVGAREIGYLFQYKRI 213  
DB 125 KGSGSDFDPKGSDAEVMRFCQSFMTLQRIHSYVDVPAGDIGVGAREIGYLFQYKRI 184  
QY 214 TKNTYGVLTTPKGQYGGSEIRPEATGYGAVLFVENVLKDGESLKGKCLVSGAGNVAQY 273  
DB 185 SNQFTSVLTGKMTYGGSLIRPEATGYGCVYFAEEMLRKREQTVGEKRVATSGGNVAQY 244  
QY 274 CAELLEKGAIVLSLSDSGYVVEPNFTREQLQAVQDMKKNSARISEYKSDTAVVVG 333  
DB 245 AARKVMDLGGKVISLSDEGTYCEAGLSESEQLWALLELKNVKR-GRISELAGQGLEFR 303  
QY 334 DRKPKWELDCQVDIAFPQCATQNEIDEHDAELLIKHGCOYVVEGANMPSTNEAIHKYNKAG 393  
DB 304 AGQLPWSLPC--DIALPCATQNELDAESARTLLRNGCVCVAEGANMPTTLEAVDIFIEAG 361  
QY 394 ILYCPGKAANAGGAVVSGLEMTQNRMSLNTWTRREEVDRDKLERIMKDIYDSAM--PSRRYV 452  
DB 362 ILFAPGKASNAGGAVVSGLEMSQNRMLLWTAGVDSKLNIMQSIHACHVHYGEENGRI 421  
QY 453 DLAAGANIAGFTKVDADVAKQAGV 476  
DB 422 INYVKGANIAGFVKVADAMLAQGVV 445

Search completed: September 8, 2005, 02:38:57

Job time : 91.0685 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 8, 2005, 02:01:27 ; Search time 25.4942 Seconds  
(without alignments)  
1393.764 Million cell updates/sec

Title: US-10-627-886-26  
Perfect score: 2465  
Sequence: 1 MDATTGDTALQKAVKQMAT.....GANIAGFTKVADAVKQAGAV 476

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/prodata/1/iaa/5A COMB.pep.\*  
2: /cgn2\_6/prodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/prodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/prodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/prodata/1/iaa/PCTUS COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Query Match | Length | ID                     | Description       |
|------------|--------|-------------|--------|------------------------|-------------------|
| 1          | 2465   | 100.0       | 476    | 2 US-08-541-033A-26    | Sequence 26, Appl |
| 2          | 2465   | 100.0       | 476    | 2 US-08-828-451-26     | Sequence 26, Appl |
| 3          | 2465   | 100.0       | 487    | 2 US-08-541-033A-24    | Sequence 24, Appl |
| 4          | 2465   | 100.0       | 487    | 2 US-08-828-451-24     | Sequence 24, Appl |
| 5          | 2465   | 100.0       | 512    | 2 US-08-541-033A-4     | Sequence 4, Appl  |
| 6          | 2465   | 100.0       | 512    | 2 US-08-828-451-4      | Sequence 4, Appl  |
| 7          | 2465   | 100.0       | 526    | 2 US-08-541-033A-2     | Sequence 2, Appl  |
| 8          | 2465   | 100.0       | 526    | 2 US-08-828-451-2      | Sequence 2, Appl  |
| 9          | 1309   | 53.1        | 467    | 4 US-09-252-991A-20646 | Sequence 20646, A |
| 10         | 1257.5 | 51.0        | 450    | 4 US-09-328-352-5725   | Sequence 5725, Ap |
| 11         | 1234.5 | 50.1        | 448    | 4 US-09-134-000C-3884  | Sequence 3884, Ap |
| 12         | 1221   | 49.5        | 448    | 4 US-09-583-110-4489   | Sequence 4489, Ap |
| 13         | 1201   | 48.7        | 447    | 2 US-08-886-640-3      | Sequence 3, Appl  |
| 14         | 1201   | 48.7        | 447    | 3 US-08-884-235-11     | Sequence 11, Appl |
| 15         | 1200   | 48.7        | 447    | 1 US-08-370-193A-11    | Sequence 11, Appl |
| 16         | 1191   | 48.3        | 452    | 4 US-09-489-039A-7937  | Sequence 7937, Ap |
| 17         | 1177.5 | 47.8        | 446    | 4 US-09-543-681A-6657  | Sequence 6657, Ap |
| 18         | 1177   | 47.7        | 447    | 3 US-08-508-761B-6     | Sequence 6, Appl  |
| 19         | 1147   | 46.5        | 461    | 3 US-09-171-337A-5     | Sequence 5, Appl  |
| 20         | 1147   | 46.5        | 461    | 4 US-09-631-022-5      | Sequence 5, Appl  |
| 21         | 1143   | 46.4        | 459    | 1 US-08-831-753-1      | Sequence 1, Appl  |
| 22         | 1037.5 | 42.1        | 454    | 4 US-09-538-092-767    | Sequence 767, App |
| 23         | 1012   | 41.1        | 368    | 4 US-09-107-433-4041   | Sequence 4041, Ap |
| 24         | 788.5  | 32.0        | 298    | 4 US-09-248-796A-17483 | Sequence 17483, A |
| 25         | 552.5  | 22.4        | 420    | 3 US-09-134-001C-3103  | Sequence 3103, Ap |
| 26         | 537.5  | 21.8        | 374    | 4 US-09-710-279-2162   | Sequence 2162, Ap |
| 27         | 537    | 21.8        | 509    | 4 US-09-902-540-11352  | Sequence 11352, A |

|    |       |      |      |                        |                   |
|----|-------|------|------|------------------------|-------------------|
| 28 | 519   | 21.1 | 420  | 3 US-09-239-303-9      | Sequence 9, Appl  |
| 29 | 482.5 | 19.6 | 409  | 4 US-09-902-540-12638  | Sequence 12638, A |
| 30 | 476.5 | 19.3 | 421  | 3 US-09-239-303-2      | Sequence 2, Appl  |
| 31 | 458.5 | 18.6 | 427  | 4 US-09-328-352-6130   | Sequence 6130, Ap |
| 32 | 441   | 17.9 | 432  | 4 US-09-489-039A-13935 | Sequence 13935, A |
| 33 | 385   | 15.6 | 87   | 2 US-08-461-990B-22    | Sequence 22, Appl |
| 34 | 368   | 14.9 | 87   | 2 US-08-461-990B-20    | Sequence 20, Appl |
| 35 | 364.5 | 14.8 | 558  | 4 US-09-538-092-1153   | Sequence 1153, Ap |
| 36 | 357   | 14.5 | 87   | 2 US-08-461-990B-23    | Sequence 23, Appl |
| 37 | 357   | 14.5 | 558  | 4 US-09-538-092-832    | Sequence 832, App |
| 38 | 357   | 14.5 | 575  | 4 US-09-949-016-7622   | Sequence 7622, Ap |
| 39 | 357   | 14.5 | 575  | 4 US-09-248-796A-17482 | Sequence 7623, Ap |
| 40 | 346   | 14.0 | 176  | 4 US-09-949-016-7623   | Sequence 17482, A |
| 41 | 168   | 6.8  | 87   | 2 US-08-461-990B-21    | Sequence 21, Appl |
| 42 | 157.5 | 6.4  | 366  | 2 US-08-804-699-2      | Sequence 2, Appl  |
| 43 | 139.5 | 5.7  | 356  | 2 US-08-461-990B-2     | Sequence 2, Appl  |
| 44 | 132   | 5.4  | 1092 | 4 US-09-538-092-122    | Sequence 122, App |
| 45 | 131   | 5.3  | 351  | 4 US-09-198-452A-991   | Sequence 991, App |

ALIGNMENTS

RESULT 1

US-08-541-033A-26  
; Sequence 26, Application US/08541033A  
; Patent No. 5879941  
; GENERAL INFORMATION:  
; APPLICANT: Schmidt, Robert R.  
; APPLICANT: Miller, Philip  
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
; TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE  
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/541.033A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Whitlock, Ted W.  
; REGISTRATION NUMBER: 36,965  
; REFERENCE/DOCKET NUMBER: UF155  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (904) 375-8100  
; TELEFAX: (904) 372-5800  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 476 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-541-033A-26

Query Match 100.0%; Score 2465; DB 2; Length 476;  
Best Local Similarity 100.0%; Pred. No. 7.2e-225;  
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDATTGDTALQKAVKQMATKAGTGLVHGINKNPVROLITLTFMKDPEQEFMQAVREV 60  
DB 1 MDATTGDTALQKAVKQMATKAGTGLVHGINKNPVROLITLTFMKDPEQEFMQAVREV 60



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| 61  | Qy | AVSLQPVFEKRPBELLPIPKQIVPEBVRTITFRVSWLLDAGNLQVNRGRFVQYSSAIGPYKG | 120 |
|     |    |  |     |
| 61  | Db | AVSLQPVFEKRPBELLPIPKQIVPEBVRTITFRVSWLLDAGNLQVNRGRFVQYSSAIGPYKG | 120 |
|     |    |  |     |
| 121 | Qy | GURFHPSVNLSTMKFLAPEQIFKNSLTTLPMGGGKGGSDFDPKGSDAEVMRFCSQPMTE    | 180 |
|     |    |  |     |
| 121 | Db | GURFHPSVNLSTMKFLAPEQIFKNSLTTLPMGGGKGGSDFDPKGSDAEVMRFCSQPMTE    | 180 |
|     |    |  |     |
| 181 | Qy | LQRHSHSYVDQVPAGDIGVCAREBIGYLFQCYKRITKNTYGLTPKGQBYGGSEIRPEATCY  | 240 |
|     |    |  |     |
| 181 | Db | LQRHSHSYVDQVPAGDIGVCAREBIGYLFQCYKRITKNTYGLTPKGQBYGGSEIRPEATCY  | 240 |
|     |    |  |     |
| 241 | Qy | GAVLFVENYLVKDGESLKGKRCLVSGAGNVAQYCAELLLLEKGAIVLSLSDSQGYVYPENG  | 300 |
|     |    |  |     |
| 241 | Db | GAVLFVENYLVKDGESLKGKRCLVSGAGNVAQYCAELLLLEKGAIVLSLSDSQGYVYPENG  | 300 |
|     |    |  |     |
| 301 | Qy | FTREQLOAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAPPCATONEIDSH   | 360 |
|     |    |  |     |
| 301 | Db | FTREQLOAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAPPCATONEIDSH   | 360 |
|     |    |  |     |
| 361 | Qy | DAELLIKHGCGQYVVEGANMPTNEAIHKYNKAGIICYCPGKAANAGGVAVSGLEMTQNRMS  | 420 |
|     |    |  |     |
| 361 | Db | DAELLIKHGCGQYVVEGANMPTNEAIHKYNKAGIICYCPGKAANAGGVAVSGLEMTQNRMS  | 420 |
|     |    |  |     |
| 421 | Qy | LNWTRTEEVDRKLERIMKDIYOSAGPSPRRYVNDILAAGANTAGTFTKVADAVKAQAV     | 476 |
|     |    |  |     |
| 421 | Db | LNWTRTEEVDRKLERIMKDIYOSAGPSPRRYVNDILAAGANTAGTFTKVADAVKAQAV     | 476 |
|     |    |  |     |

## RESULT 2

```

US-08-828-451-26
/ Sequence 26, Application US/08828451
/ Patent No. 5985634
/ GENERAL INFORMATION:
/ APPLICANT: Schmidt, Robert R.
/ APPLICANT: Miller, Philip
/ TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
/ TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
/ TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
/ NUMBER OF SEQUENCES: 26
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Saliwanchik & Saliwanchik
/ STREET: 2421 N.W. 41st Street, Suite A-1
/ CITY: Gainesville
/ STATE: Florida
/ COUNTRY: USA
/ ZIP: 32606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/828,451
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/541,033
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Whitlock, Ted W.
/ REGISTRATION NUMBER: 36,965
/ REFERENCE/DOCKET NUMBER: UF155
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (904) 375-8100
/ TELEFAX: (904) 372-5800
/ INFORMATION FOR SEQ ID NO: 26:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 476 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-828-451-26

```

| Query Match                  | 100.0%;  | Score 2465;         | DB 2;   | Length 476; |
|------------------------------|--|---------------------|---------|-------------|
| Best Local Similarity        | 100.0%;  | Pred. No. 7.2e-225; |         |             |
| Matches 476; Conservative 0; | Mismatches 0;  | Indels 0;           | Gaps 0; |             |
| Qy 1                         | MDATTGGDTALQAKAVQKMATKAGTEGLVHGINKPDPVRLQLTETFMKDPQOQBPMQAVREV   |                     |         |             |
| Db 1                         | MDATTGGDTALQAKAVQKMATKAGTEGLVHGINKPDPVRLQLTETFMKDPQOQBPMQAVREV   |                     |         |             |
| Qy 61                        | AVSLQVPFKRPELLPIFKQIVPEPERVITFRVSWLDDAGNLQVNRGRFRVOYSSAIGPYKGG   |                     |         |             |
| Db 61                        | AVSLQVPFKRPELLPIFKQIVPEPERVITFRVSWLDDAGNLQVNRGRFRVOYSSAIGPYKGG   |                     |         |             |
| Qy 121                       | GLRFPHSPVNLISIMKFLAFBQIPKNSLTTLTPMGGGKGGSDFPDKGKSDAEVMPFCQSPMTET |                     |         |             |
| Db 121                       | GLRFPHSPVNLISIMKFLAFBQIPKNSLTTLTPMGGGKGGSDFPDKGKSDAEVMPFCQSPMTET |                     |         |             |
| Qy 181                       | LQRHISYVDVPAGDIGVGAREIGYLFQGYKGRITKNYTVGLTPKQGEYCGSSEIRPEATGY    |                     |         |             |
| Db 181                       | LQRHISYVDVPAGDIGVGAREIGYLFQGYKGRITKNYTVGLTPKQGEYCGSSEIRPEATGY    |                     |         |             |
| Qy 241                       | GAVLFVENVLKDKGESLKGKRCILVSGAGNVAQYCAELLLEKGAIVLSLSDSQSYVYEPNG    |                     |         |             |
| Db 241                       | GAVLFVENVLKDKGESLKGKRCILVSGAGNVAQYCAELLLEKGAIVLSLSDSQSYVYEPNG    |                     |         |             |
| Qy 301                       | FTREQLQAVQDMKKKNSNARISEYKSDTAVYVGDRRKPMELDCQVDIAFPCATQNEIDBHE    |                     |         |             |
| Db 301                       | FTREQLQAVQDMKKKNSNARISEYKSDTAVYVGDRRKPMELDCQVDIAFPCATQNEIDBHE    |                     |         |             |
| Qy 361                       | DAELLTIKHGCOYVVEGANPSTNEATHKNYKAGIIYCPGKAANAGVAVSLGLEMTQNRMS     |                     |         |             |
| Db 361                       | DAELLTIKHGCOYVVEGANPSTNEATHKNYKAGIIYCPGKAANAGVAVSLGLEMTQNRMS     |                     |         |             |
| Qy 421                       | LNNTRVEVDKLERIMKQIYDSAMGSPRRYNDLAAGANIAGTPTKVDAAVKQAGAV 476      |                     |         |             |
| Db 421                       | LNNTRVEVDKLERIMKQIYDSAMGSPRRYNDLAAGANIAGTPTKVDAAVKQAGAV 476      |                     |         |             |

### RESULT 3

RESOLUTION 3  
US-08-541-033A-24  
; Sequence 24, Application US/08541033A  
; Patent No. 5879941  
; GENERAL INFORMATION:  
; APPLICANT: Schmidt, Robert R.  
; APPLICANT: Miller, Philip  
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
; RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE  
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/541,033A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Whitlock, Ted W.  
; REGISTRATION NUMBER: 36,965  
; REFERENCE/DOCKET NUMBER: UFI55  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (904) 375-8100  
; TELEFAX: (904) 372-5800  
; INFORMATION FOR SEQ ID NO: 24:

```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-541-033A-24

Query Match      100.0%; Score 2465; DB 2; Length 487;
Best Local Similarity 100.0%; Pred. No. 7.5e-225;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKPDPVROLLTEIFMKDPQOEPMQAVREV 60
DB 12 MDATTGDTALQKAVKQMATKAGTEGLVHGINKPDPVROLLTEIFMKDPQOEPMQAVREV 71

QY 61 AVSLQPVFEKRPPELLPIFKQIVPEPVIITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
DB 72 AVSLQPVFEKRPPELLPIFKQIVPEPVIITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 131

QY 121 GLRFHPSVNLISIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMPFCQSFMT 180
DB 132 GLRFHPSVNLISIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMPFCQSFMT 191

QY 181 LQRHISYVDVPAGDIGVGAREIGYLFQYKRTKNTYGVLTGTPKGQYGGSEIRPEATGY 240
DB 192 LQRHISYVDVPAGDIGVGAREIGYLFQYKRTKNTYGVLTGTPKGQYGGSEIRPEATGY 251

QY 241 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQYVYEPNG 300
DB 252 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQYVYEPNG 311

QY 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCCATQNEIDSH 360
DB 312 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCCATQNEIDSH 371

QY 361 DAELLIKHGQYVVEGANPNSTNEAIHKYNKAGIIVCPGKAANAGGAVVSGLEMTQNRMS 420
DB 372 DAELLIKHGQYVVEGANPNSTNEAIHKYNKAGIIVCPGKAANAGGAVVSGLEMTQNRMS 431

QY 421 LNWTRVEVRDKLERIMKDIYDSAMGSPRRYVNDLAAGANIAGFTTKVADAVKAQGA 476
DB 432 LNWTRVEVRDKLERIMKDIYDSAMGSPRRYVNDLAAGANIAGFTTKVADAVKAQGA 487
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RESULT 4
US-08-828-451-24
; Sequence 24, Application US/08828451
; Patent No. 5985634
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,451
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,033
```

```
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UFI155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-828-451-24

Query Match      100.0%; Score 2465; DB 2; Length 487;
Best Local Similarity 100.0%; Pred. No. 7.5e-225;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKPDPVROLLTEIFMKDPQOEPMQAVREV 60
DB 12 MDATTGDTALQKAVKQMATKAGTEGLVHGINKPDPVROLLTEIFMKDPQOEPMQAVREV 71

QY 61 AVSLQPVFEKRPPELLPIFKQIVPEPVIITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
DB 72 AVSLQPVFEKRPPELLPIFKQIVPEPVIITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 131

QY 121 GLRFHPSVNLISIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMPFCQSFMT 180
DB 132 GLRFHPSVNLISIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMPFCQSFMT 191

QY 181 LQRHISYVDVPAGDIGVGAREIGYLFQYKRTKNTYGVLTGTPKGQYGGSEIRPEATGY 240
DB 192 LQRHISYVDVPAGDIGVGAREIGYLFQYKRTKNTYGVLTGTPKGQYGGSEIRPEATGY 251

QY 241 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQYVYEPNG 300
DB 252 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQYVYEPNG 311

QY 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCCATQNEIDSH 360
DB 312 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCCATQNEIDSH 371

QY 361 DAELLIKHGQYVVEGANPNSTNEAIHKYNKAGIIVCPGKAANAGGAVVSGLEMTQNRMS 420
DB 372 DAELLIKHGQYVVEGANPNSTNEAIHKYNKAGIIVCPGKAANAGGAVVSGLEMTQNRMS 431

QY 421 LNWTRVEVRDKLERIMKDIYDSAMGSPRRYVNDLAAGANIAGFTTKVADAVKAQGA 476
DB 432 LNWTRVEVRDKLERIMKDIYDSAMGSPRRYVNDLAAGANIAGFTTKVADAVKAQGA 487
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RESULT 5
US-08-541-033A-4
; Sequence 4, Application US/08541033A
; Patent No. 5879941
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,033A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UF155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 512 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-541-033A-4

```

Query Match 100.0%; Score 2465; DB 2; Length 512;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-225;  
 Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKPDPVRLQLLTFIMKDPQEQEFMQAVREV 60
DB 37 MDATTGDTALQKAVKQMATKAGTEGLVHGINKPDPVRLQLLTFIMKDPQEQEFMQAVREV 96
QY 61 AVSLQPVPEKPELLPIFKQIVPEPVTITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
DB 97 AVSLQPVPEKPELLPIFKQIVPEPVTITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 156
QY 121 GLRFHPSVNLISIMKFLAFEQIFKNSLTTLPMGGGKGSDFDPKGSKSDAEVWRFCSFMTE 180
DB 157 GLRFHPSVNLISIMKFLAFEQIFKNSLTTLPMGGGKGSDFDPKGSKSDAEVWRFCSFMTE 216
QY 181 LQRHISYVDVPAGDIGVAREIGYLFQYKRIITKNYTVGLTPKGQYGGSEIRPEATGY 240
DB 217 LQRHISYVDVPAGDIGVAREIGYLFQYKRIITKNYTVGLTPKGQYGGSEIRPEATGY 276
QY 241 GAVLFVENVLKDGESLKGKRCVSGAGNVAQYCAELLLKGAIVLSLSDSGYVYEPNG 300
DB 277 GAVLFVENVLKDGESLKGKRCVSGAGNVAQYCAELLLKGAIVLSLSDSGYVYEPNG 336
QY 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRLKRWELDCQVDIAPPATQNEIDEH 360
DB 337 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRLKRWELDCQVDIAPPATQNEIDEH 396
QY 361 DAELLIKHGCGQYVVEGANNPSTNEAIHKYNKAGIICPGKAANAGGAVVSGLEMTQNRMS 420
DB 397 DAELLIKHGCGQYVVEGANNPSTNEAIHKYNKAGIICPGKAANAGGAVVSGLEMTQNRMS 456
QY 421 LNWTRREEVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGV 476
DB 457 LNWTRREEVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGV 512

```

RESULT 6  
 US-08-828-451-4  
 ; Sequence 4, Application US/08828451  
 ; Patent No. 5985634  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schmidt, Robert R.  
 ; APPLICANT: Miller, Philip  
 ; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
 ; TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE  
 ; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE  
 ; NUMBER OF SEQUENCES: 26  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Saliwanchik & Saliwanchik  
 ; STREET: 2421 N.W. 41st Street, Suite A-1

```

; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,451
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,033
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UF155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 512 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-828-451-4

```

Query Match 100.0%; Score 2465; DB 2; Length 512;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-225;  
 Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKPDPVRLQLLTFIMKDPQEQEFMQAVREV 60
DB 37 MDATTGDTALQKAVKQMATKAGTEGLVHGINKPDPVRLQLLTFIMKDPQEQEFMQAVREV 96
QY 61 AVSLQPVPEKPELLPIFKQIVPEPVTITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
DB 97 AVSLQPVPEKPELLPIFKQIVPEPVTITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 156
QY 121 GLRFHPSVNLISIMKFLAFEQIFKNSLTTLPMGGGKGSDFDPKGSKSDAEVWRFCSFMTE 180
DB 157 GLRFHPSVNLISIMKFLAFEQIFKNSLTTLPMGGGKGSDFDPKGSKSDAEVWRFCSFMTE 216
QY 181 LQRHISYVDVPAGDIGVAREIGYLFQYKRIITKNYTVGLTPKGQYGGSEIRPEATGY 240
DB 217 LQRHISYVDVPAGDIGVAREIGYLFQYKRIITKNYTVGLTPKGQYGGSEIRPEATGY 276
QY 241 GAVLFVENVLKDGESLKGKRCVSGAGNVAQYCAELLLKGAIVLSLSDSGYVYEPNG 300
DB 277 GAVLFVENVLKDGESLKGKRCVSGAGNVAQYCAELLLKGAIVLSLSDSGYVYEPNG 336
QY 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRLKRWELDCQVDIAPPATQNEIDEH 360
DB 337 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRLKRWELDCQVDIAPPATQNEIDEH 396
QY 361 DAELLIKHGCGQYVVEGANNPSTNEAIHKYNKAGIICPGKAANAGGAVVSGLEMTQNRMS 420
DB 397 DAELLIKHGCGQYVVEGANNPSTNEAIHKYNKAGIICPGKAANAGGAVVSGLEMTQNRMS 456
QY 421 LNWTRREEVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGV 476
DB 457 LNWTRREEVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGV 512

```

RESULT 7  
 US-08-541-033A-2  
 ; Sequence 2, Application US/08541033A  
 ; Patent No. 5879941  
 ; GENERAL INFORMATION:

```

; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,033A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UF155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 526 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-541-033A-2

Query Match 100.0%; Score 2465; DB 2; Length 526;
Best Local Similarity 100.0%; Pred. No. 8.4e-225;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKNPDPVRLLTETFMKDPQQSFMOAVREV 60
Db 51 MDATTGDTALQKAVKQMATKAGTEGLVHGINKNPDPVRLLTETFMKDPQQSFMOAVREV 110
Qy 61 AVSLQPVFEKREPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
Db 111 AVSLQPVFEKREPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 170
Qy 121 GLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFPKGSDAEVMRFQCSFMTE 180
Db 171 GLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFPKGSDAEVMRFQCSFMTE 230
Qy 181 LQRHSYVQDVPAGDIGVGAREIGYLFQYKRIITKNYTGVLTPKQEGYGGSEIRPEATGY 240
Db 231 LQRHSYVQDVPAGDIGVGAREIGYLFQYKRIITKNYTGVLTPKQEGYGGSEIRPEATGY 290
Qy 241 GAVLFVENVLKDKGESLKGKRCCLVSGAGNVAQYCAELLLKGAIVLSLSDSGQYVYEPNG 300
Db 291 GAVLFVENVLKDKGESLKGKRCCLVSGAGNVAQYCAELLLKGAIVLSLSDSGQYVYEPNG 350
Qy 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDGRRKPWELDCQVDIAPPCATQNEIDEH 360
Db 351 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDGRRKPWELDCQVDIAPPCATQNEIDEH 410
Qy 361 DAELLIKGCQYVVEGANPSTNEAIIHKYKAGIIPCOKAANAGGAVVSGLEMTQNRMS 420
Db 411 DAELLIKGCQYVVEGANPSTNEAIIHKYKAGIIPCOKAANAGGAVVSGLEMTQNRMS 470
Qy 421 LNWTRREVRDKLERIMKDIYDSAMGPSREYVNDLAAGANIAGFTKVADAVKAGGAV 476
Db 471 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAGGAV 526
```

```

RESULT 8
US-08-828-451-2
; Sequence 2, Application US/08028451
; Patent No. 5985634
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,451
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,033
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UF155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 526 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-828-451-2
```

```

Query Match 100.0%; Score 2465; DB 2; Length 526;
Best Local Similarity 100.0%; Pred. No. 8.4e-225;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKNPDPVRLLTETFMKDPQQSFMOAVREV 60
Db 51 MDATTGDTALQKAVKQMATKAGTEGLVHGINKNPDPVRLLTETFMKDPQQSFMOAVREV 110
Qy 61 AVSLQPVFEKREPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
Db 111 AVSLQPVFEKREPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 170
Qy 121 GLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFPKGSDAEVMRFQCSFMTE 180
Db 171 GLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFPKGSDAEVMRFQCSFMTE 230
Qy 181 LQRHSYVQDVPAGDIGVGAREIGYLFQYKRIITKNYTGVLTPKQEGYGGSEIRPEATGY 240
Db 231 LQRHSYVQDVPAGDIGVGAREIGYLFQYKRIITKNYTGVLTPKQEGYGGSEIRPEATGY 290
Qy 241 GAVLFVENVLKDKGESLKGKRCCLVSGAGNVAQYCAELLLKGAIVLSLSDSGQYVYEPNG 300
Db 291 GAVLFVENVLKDKGESLKGKRCCLVSGAGNVAQYCAELLLKGAIVLSLSDSGQYVYEPNG 350
Qy 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDGRRKPWELDCQVDIAPPCATQNEIDEH 360
Db 351 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDGRRKPWELDCQVDIAPPCATQNEIDEH 410
```

QY 361 DAELLIKHGCQVVEGANPSTNEAIHKYNKAGIICPGKAANAGVAVSGLEMTQNRMS 420  
DB 411 DAELLIKHGCQVVEGANPSTNEAIHKYNKAGIICPGKAANAGVAVSGLEMTQNRMS 470  
QY 421 LNWTRVEVRDKLERIMKDIYDSAMPSSRRYNDLAAGANIAGFTKVADAVKAQAV 476  
DB 471 LNWTRVEVRDKLERIMKDIYDSAMPSSRRYNDLAAGANIAGFTKVADAVKAQAV 526

## RESULT 9

US-09-252-991A-20646  
; Sequence 20646, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 20646  
; LENGTH: 450  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-20646

Query Match 53.1%; Score 1309; DB 4; Length 450;  
Best Local Similarity 59.2%; Pred. No. 2.5e-115;  
Matches 263; Conservative 55; Mismatches 120; Indels 6; Gaps 4;

QY 36 VRLQLTEIFPKDPEQEFMQAVREAVSLQVPEKPELLP--IPKQIPEPERVITFRVS 93  
DB 10 VDAFLERLKRDPDPQEPFQAEEVLRSLWPFLEANPHYLEAGIIEIVEPERAILFRVP 69  
QY 94 WDDAGNLQVNRGFRVQYSSAIGPYKGGRLRPHPSVNLSTIMKFLAPEQIFKNSLTLLPMGG 153  
DB 70 WDDQGRVRNRGFRVQYSSAIGPYKGGRLRPHPSVNLSTIMKFLAPEQIFKNSLTLLPMGG 129  
QY 154 KGGSDPDPKGSDAEVRMFCQSFMTLQRIHISYVDVPAGDIGVGAIRGIVLFGQYKRI 213  
DB 130 KGGSDPDPKGSDAEVRMFCQSFMSLYRHVGADLDVPAGDIGVGAIRGIVLFGQYKRL 189  
QY 214 TKNYTGVLTPKQEGYGGSEIRPEATGYGAVLFVENVLKDGESLKGKCLVSGAGNVAQY 273  
DB 190 SNQFTSVLTGKLSYGSLIRPEATGYGAVLFVENVLKDGESLKGKCLVSGAGNVAQY 249  
QY 274 CASLLEKGAIVLSLSDSGYVYEPNGFTREQLQAVQDMKKNNGARISEYKSDTAVTVVG 333  
DB 250 AARKVMGEMGVISLSDSGYVYEPNGFTREQLQAVQDMKKNNGARISEYKSDTAVTVVG 308  
QY 334 DRKPWELDCQVDIAPPCATONEIDHDAELLIKHGCQVVEGANPSTNEAIHKYNKAG 393  
DB 309 EGRRPWGLAC--DIALPCATONELDAEDARRLLANGCVCAEAGNMPSTLEAVDLFLEAG 366  
QY 394 IYCPGKAANAGVAVSGLEMTQNRMSLNWTRVEVRDKLERIMKDIYDSA-MGPSRRYNV 452  
DB 367 ILIYAPKASNAGVAVSGLEMTQNRMSLNWTRVEVRDKLERIMKDIYDSA-MGPSRRYNV 426  
QY 453 ILAAGANIAGFTKVADAVKAQAV 476  
DB 427 NVYKGANIAGFTKVADAVKAQAV 450

## RESULT 10

US-09-328-352-5725  
; Sequence 5725, Application US/09328352  
; Patent No. 6562958

## ; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
; CURRENT APPLICATION NUMBER: US/09/328.352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 5725  
; LENGTH: 467  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-5725

Query Match 51.0%; Score 1257.5; DB 4; Length 467;  
Best Local Similarity 55.9%; Pred. No. 2e-110;  
Matches 256; Conservative 61; Mismatches 128; Indels 13; Gaps 5;  
QY 27 LVH-----GINKPDPVRLQLTEIFPKDPEQEFMQAVREAVSLQVPEKPELLP--IP 78  
DB 11 LIHYAEDRALKYNNLNEFLNYVQARDPHQPEFLQAVEEVMNTSLWPFIEKXNPEYABOQSL 70  
QY 79 KOIPEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGGRLRPHPSVNLSTIMKFLAF 138  
DB 71 ERLVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGGRLRPHPSVNLSTIMKFLAF 130  
QY 139 EOIPEKNSLTLLPMGGGKGSDFDPKGSDAEVRMFCQSFMTLQRIHISYVDVPAGDIGV 198  
DB 131 EOTFKNSLTLLPMGGGKGSDFDPKGSDAEVRMFCQSFMTLQRIHISYVDVPAGDIGV 190  
QY 199 GARIGVILFGQYKRIHISYVDVPAGDIGV 258  
DB 191 GARVGYVMAGMMKKLSNDTACVFTGKISFGGSLMRPEATGYGVYFABEMLKTRGQSFA 250  
QY 259 GKRCVLSGAGNVAQYCAELLEKGAIVLSLSDSGYVYEPNGFTREQLQAVQDMKKNNKS 318  
DB 251 KGTVSISSGNGNVAQYAAEKAMFLGAKVVTLSDSNGTVLKGFTDELLAEVWELKNIKR- 309  
QY 319 ARISEYKSDTAVTVGDRRKPWELDCQVDIAPPCATONEIDHDAELLIKHGCQVVEGAN 378  
DB 310 GRISFASKKHGFYEPGKTPWHI--PVDIALPCATONELTGEDAKTLIANGVICVAEGAN 367  
QY 379 MPSTNEAIHKYNKAGIICPGKAANAGVAVSGLEMTQNRMSLNWTRVEVRDKLERIMKD 438  
DB 368 MPSTLEAVEHFEAKILYAPKASNAGVAVSGLEMTQNRMSLNWTRVEVRDKLERIMKD 427  
QY 439 IYDSAM--GPSRRYNVDLAAGANIAGFTKVADAVKAQ 474  
DB 428 IHANCVRYGTKEGTVNYVDGANIAGFTKVADAVKAQ 465

## RESULT 11

US-09-134-000C-3884  
; Sequence 3884, Application US/09134000C  
; Patent No. 6617156  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; FILE REFERENCE: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS  
; CURRENT APPLICATION NUMBER: US/09/134.000C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/055,778  
; PRIOR FILING DATE: 1997-08-15  
; NUMBER OF SEQ ID NOS: 6812  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 3884  
; LENGTH: 448  
; TYPE: PRT  
; ORGANISM: Enterococcus faecalis  
US-09-134-000C-3884

Query Match 50.1%; Score 1234.5; DB 4; Length 448;







```
; LENGTH: 447 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-370-193A-11

Query Match      48.7%; Score 1200; DB 1; Length 447;
Best Local Similarity 54.0%; Pred. No. 5.4e-105;
Matches 241; Conservative 67; Mismatches 128; Indels 10; Gaps 5;

QY 36 VRQLLTETFMKQPEQOEQAVREAVASLQPVFEKPEL--LPFVKQIVEPERVITFRYS 93
Db 7 LESFLNHVQKRDNQTEFAQAVREVTTLWFFLEQMPKYRQMSLLERLVEPERVIOFRVV 66

QY 94 WLDAGNLQVNRGRVQYSSAIGPYKGLRFHPSVNLISIMKFLAFQIIFKNSLTTLPMGG 153
Db 67 WVDNRQIQVNRARWQFSSAIGPYKGMRFHPSVNLISILKFLGFQTFKNALTTLPMGG 126

QY 154 GKGGSDPDKGKSDAEVWRFCQSFMTLQRHISYVQDVPAQDIGVGAKEIGYLFQYKRI 213
Db 127 GKGGSDPDKGKSEGEVMRFQCALMTELYRHLGADTDVPAGDIGVGGREVGFMAGNMKKL 186

QY 214 TKNYTGVLTQKQOEYGSSEIRPEATGYGAVLFVENVLKDKGESLKGKRCILVSGAGNVAQY 273
Db 187 SNTACVFTGKGLUSFGGSLIRPEATGYGLVYFTTEAMLKRHGMFGEMRVSVSGSGNVAQY 246

QY 274 CAELLEKGAIVLSLSDSQYVYEPNGFTREQQAQVQDMKKKNNSARISEYKSDTAVVYG 333
Db 247 AIEKAMEFGARVITASDSSGTVVDESQFTYKEKLARLIEI-KASRDGRVADYAKEFGLVYL 305

QY 334 DRKRWELDCQVDIAPPCATQNEIDEHDAELLIKHCQCYVVEGANNPSTNEAIHKYNKAG 393
Db 306 EGQOPWNL--PVDIALPCATQNELDVAHQLIANGVKAVAEGANNPPTTEATLFPQQAG 363

QY 394 IIVCPGKAANAGGAVVSGLEMTQNRMSLNWTRVEVRDKLERIMKDIYDSAM---GPSRRY 450
Db 364 VLFAPGAANAGGVATSGLEMPQNAARLGWKAQKVDARLHHIMLDIHHACVHGGEGEQT 423

QY 451 NYDLAAGANIAGFTKVADAVKQAGAV 476
Db 424 N--YVQGANIAGFVKVADAMLAQGVI 447
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Search completed: September 8, 2005, 02:12:08  
Job time : 26.4942 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 8, 2005, 02:12:18 ; Search time 86.1641 Seconds  
(without alignments)  
2828.902 Million cell updates/sec

Title: US-10-627-886-26  
Perfect score: 2465  
Sequence: 1 MDATTGDTALQKAVQMAT.....GANTAGFTKVDVAKQAGAV 476

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID        | Description        |
|------------|--------|-------------|--------|--------------|--------------------|
| 1          | 2444   | 99.1        | 523    | 1 DHE4_CHLSD | P28998 chlorella s |
| 2          | 1375   | 55.8        | 510    | 2 Q8ILF7     | Q8ILF7 plasmodium  |
| 3          | 1361   | 55.2        | 1203   | 2 Q7RQ39     | Q7RQ39 plasmodium  |
| 4          | 1328   | 53.9        | 446    | 2 Q7YZU9     | Q7YZU9 spiroplasma |
| 5          | 1327.5 | 53.9        | 449    | 2 Q7R3N7     | Q7R3N7 giardia lam |
| 6          | 1324.5 | 53.7        | 449    | 1 DHE4_GIALA | P28724 giardia lam |
| 7          | 1309   | 53.1        | 445    | 2 Q8HVJ7     | Q8HVJ7 pseudomonas |
| 8          | 1300.5 | 52.8        | 444    | 2 Q9JY71     | Q9JY71 neisseria m |
| 9          | 1294.5 | 52.5        | 444    | 2 Q9JY56     | Q9JY56 neisseria m |
| 10         | 1287.5 | 52.2        | 449    | 2 Q8RQ23     | Q8RQ23 pseudomonas |
| 11         | 1285   | 52.1        | 445    | 2 Q9Z3C4     | Q9Z3C4 pseudomonas |
| 12         | 1284.5 | 52.1        | 437    | 2 Q7YZU7     | Q7YZU7 trichomonas |
| 13         | 1279.5 | 51.9        | 470    | 2 Q9G940     | Q9G940 plasmodium  |
| 14         | 1279.5 | 51.9        | 470    | 2 Q8ILT0     | Q8ILT0 plasmodium  |
| 15         | 1265   | 51.3        | 442    | 2 Q9TXS8     | Q9TXS8 plasmodium  |
| 16         | 1264   | 51.3        | 442    | 2 Q9GTX5     | Q9GTX5 plasmodium  |
| 17         | 1257   | 51.0        | 465    | 2 Q6S143     | Q6S143 uncultured  |
| 18         | 1253.5 | 50.9        | 536    | 2 Q7RGT5     | Q7RGT5 plasmodium  |
| 19         | 1250.5 | 50.7        | 448    | 2 Q8G6L0     | Q8G6L0 bifidobacte |
| 20         | 1250.5 | 50.7        | 455    | 2 Q8GE72     | Q8GE72 ruminococcu |
| 21         | 1249.5 | 50.7        | 447    | 2 Q6FD67     | Q6FD67 acinetobact |
| 22         | 1241.5 | 50.4        | 448    | 2 Q8XK85     | Q8XK85 clostridium |
| 23         | 1240.5 | 50.3        | 449    | 2 Q8S4J6     | Q8S4J6 streptococc |
| 24         | 1239.5 | 50.3        | 448    | 2 Q8J5G2     | Q8J5G2 enterococc  |
| 25         | 1238   | 50.2        | 449    | 1 DHE4_HAEIN | P43793 haemophilus |
| 26         | 1236.5 | 50.2        | 449    | 2 Q8DY77     | Q8DY77 streptococc |
| 27         | 1234   | 50.1        | 447    | 2 Q61083     | Q61083 trypanosoma |
| 28         | 1231.5 | 50.0        | 462    | 2 Q6SW57     | Q6SW57 manheimia   |
| 29         | 1230.5 | 49.9        | 449    | 2 Q8DUL2     | Q8DUL2 streptococc |
| 30         | 1230   | 49.9        | 449    | 2 Q9CPJ4     | Q9CPJ4 pasteurella |
| 31         | 1225.5 | 49.7        | 444    | 1 DHE3_BACTN | P94598 bacteroides |

|    |        |      |     |              |                    |
|----|--------|------|-----|--------------|--------------------|
| 32 | 1225   | 49.7 | 448 | 2 Q9AIW1     | Q9AIW1 streptococc |
| 33 | 1214.5 | 49.3 | 444 | 1 DHE4_PRERU | P95544 prevotella  |
| 34 | 1214   | 49.2 | 448 | 2 Q8DPG0     | Q8DPG0 streptococc |
| 35 | 1212   | 49.2 | 448 | 2 Q97QB4     | Q97QB4 streptococc |
| 36 | 1210.5 | 49.1 | 458 | 2 Q9KB34     | Q9KB34 bacillus ha |
| 37 | 1206.5 | 48.9 | 447 | 2 Q7VSN6     | Q7VSN6 bordetella  |
| 38 | 1205.5 | 48.9 | 424 | 2 Q9RTN9     | Q9RTN9 deinococcus |
| 39 | 1205.5 | 48.9 | 444 | 2 Q64Q81     | Q64Q81 bacteroides |
| 40 | 1205.5 | 48.9 | 464 | 2 Q7WEU7     | Q7WEU7 bordetella  |
| 41 | 1202   | 48.8 | 448 | 2 Q88XM9     | Q88XM9 lactobacill |
| 42 | 1201   | 48.7 | 447 | 1 DHE4_ECOLI | P00370 escherichia |
| 43 | 1200.5 | 48.7 | 446 | 2 Q6O9J6     | Q6O9J6 trypanosoma |
| 44 | 1200   | 48.7 | 449 | 2 Q6AJBI     | Q6AJBI desulfotale |
| 45 | 1199   | 48.6 | 443 | 2 Q97L29     | Q97L29 clostridium |

ALIGNMENTS

RESULT 1

|    |  |           |      |         |
|----|--|-----------|------|---------|
| ID | DHE4_CHLSD   | STANDARD; | PRT; | 523 AA. |
| AC | P28998;  |           |      |         |
| DT | 01-DEC-1992 (Rel. 24, Created)   |           |      |         |
| DT | 01-DEC-1992 (Rel. 24, Last sequence update)                                |           |      |         |
| DT | 29-MAR-2004 (Rel. 43, Last annotation update)                              |           |      |         |
| DE | NADP-specific glutamate dehydrogenase (EC 1.4.1.4) (NADP-GDH)              |           |      |         |
| DE | (Fragment).  |           |      |         |
| OS | Chlorella sorokiniana.   |           |      |         |
| OC | Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;     |           |      |         |
| OC | Chlorellaceae; Chlorella.  |           |      |         |
| NC | NCBI_TaxID=3076;   |           |      |         |
| RN | [1]  |           |      |         |
| RP | SEQUENCE FROM N.A.   |           |      |         |
| RX | MEDLINE=92032762; PubMed=1718478;  |           |      |         |
| RA | Cock J.M., Kim K.D., Miller P.W., Hutson R.G., Schmidt R.R.;               |           |      |         |
| RT | "A nuclear gene with many introns encoding ammonium-inducible              |           |      |         |
| RT | chloroplastic NADP-specific glutamate dehydrogenase(s) in Chlorella        |           |      |         |
| RT | sorokiniana.";   |           |      |         |
| RL | Plant Mol. Biol. 17:1023-1044(1991).                                       |           |      |         |
| CC | -!- CATALYTIC ACTIVITY: L-glutamate + H(2)O + NADP(+) = 2-oxoglutarate     |           |      |         |
| CC | + NH(3) + NADPH.   |           |      |         |
| CC | -!- SUBUNIT: Homo- and heterohexamers of alpha and beta subunits. Both     |           |      |         |
| CC | subunits are encoded by the same gene.                                     |           |      |         |
| CC | -!- SUBCELLULAR LOCATION: Chloroplast.                                     |           |      |         |
| CC | -!- INDUCTION: By ammonium.  |           |      |         |
| CC | -!- PTM: The N-termini of the alpha and the beta chains are blocked.       |           |      |         |
| CC | -!- SIMILARITY: Belongs to the Glu/Leu/Phe/Val dehydrogenases family.      |           |      |         |
| CC | -----  |           |      |         |
| CC | This SWISS-PROT entry is copyright. It is produced through a collaboration |           |      |         |
| CC | between the Swiss Institute of Bioinformatics and the EMBL outstation -    |           |      |         |
| CC | the European Bioinformatics Institute. There are no restrictions on its    |           |      |         |
| CC | use by non-profit institutions as long as its content is in no way         |           |      |         |
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| CC | entities requires a license agreement (see http://www.isb-sib.ch/announce/ |           |      |         |
| CC | or send an email to license@isb-sib.ch).                                   |           |      |         |
| CC | -----  |           |      |         |
| CC | EMBL; X58832; CAA41636.1; -  |           |      |         |
| DR | EMBL; X58831; CAA41635.1; ALT_SEQ.   |           |      |         |
| DR | PIR; S17949; S17949.   |           |      |         |
| DR | HSSP; P24295; LAUP.  |           |      |         |
| DR | InterPro; IPR006095; GLFV dehydrog.  |           |      |         |
| DR | InterPro; IPR006096; GLFV dehydrog_C.                                      |           |      |         |
| DR | InterPro; IPR006097; GLFV dehydrog_N.                                      |           |      |         |
| DR | Pfam; PF02028; GLFV dehydrog; 1.   |           |      |         |
| DR | Pfam; PF02812; GLFV dehydrog; 1.   |           |      |         |
| DR | PRINTS; PR00082; GLFDHGNASE.   |           |      |         |
| DR | PROSITE; PS00074; GLFV DEHYDROGENASE; 1.                                   |           |      |         |
| DR | Chloroplast; NADP; Oxidoreductase.   |           |      |         |
| FT | NON_TER 1  |           |      |         |
| FT | ACT SITE 202 202   |           |      |         |
| FT | By similarity.   |           |      |         |
| FT | SEQUENCE 523 AA; 57529 MW; A35FE730E5FE974 CRC64;                          |           |      |         |

Query Match 99.1%; Score 2444; DB 1; Length 523;  
Best Local Similarity 99.2%; Pred. No. 1.7e-163;  
Matches 472; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDATTGDFALQAVKQATKAGTGLVHGINKPDPVRLQLLTIFPKDPEQEFMQAVREV 60  
DB 48 MDATTGDFALQAVKQATKAGTGLVHGINKPDLQLLTIFPKDPEQEFMQAVREV 107

QY 61 AVSLOPVFEKRELLPIKQIIVPEPVTFRVSWLDDAGNLQVNGFRVQYSSATGPYKG 120  
DB 108 AVSLOPVFEKRELLPIKQIIVPEPVTFRVSWLDDAGNLQVNGFRVQYSSATGPYKG 167

QY 121 GLRPHPSVNLSTMKFLAEPQIFKNSLTTLPMGGGKGGSDPDKGSDAEVNRFCOSFMT 180  
DB 168 GLRPHPSVNLSTMKFLAEPQIFKNSLTTLPMGGGKGGSDPDKGSDAEVNRFCOSFMT 227

QY 181 LQRHSYVQDVPAGDIGVAREIGYLFQYKRTIKNTYGVLPKQOEGGSEIRPEATGY 240  
DB 228 LQRHSYVQDVPAGDIGVAREIGYLFQYKRTIKNTYGVLPKQOEGGSEIRPEATGY 287

QY 241 GAVLFVENVLKDGSLSKGRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQYVYEPNG 300  
DB 288 GAVLFVENVLKDGSLSKGRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQYVYEPNG 347

QY 301 FTREQLQAVQDMKKNNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAPPCATONEIDEH 360  
DB 348 FTREQLQAVQDMKKNNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAPPCATONEIDEH 407

QY 361 DAEELIKHGCGQVYVGGANPNSTNEAIHKYNKAGIICYPGKAANAGGVAVSGLEMTQNRMS 420  
DB 408 DAEELIKHGCGQVYVGGANPNSTNEAIHKYNKAGIICYPGKAANAGGVAVSGLEMTQNRMS 467

QY 421 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVDADAKQAGV 476  
DB 468 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVDADAKQAGV 523

RESULT 2  
Q8ILF7 PRELIMINARY; PRT; 510 AA.

AC Q8ILF7;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Glutamate dehydrogenase, putative.  
GN ORFNames=PF14\_0286;  
OS Plasmodium falciparum (isolate 3D7).  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=36329;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;  
RA Gardner M.J., Hall N., Nelson K.E., Bowman S., Paulsen I.T., James K.,  
RA Carlson J.M., Pail A., Fung E., White O., Bertram M., Hyman R.W.,  
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,  
RA Chan M.S., Nene V., Shallow S.J., Suh B., Peterson J., Angioli S.,  
RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,  
RA Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,  
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,  
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,  
RA Fraser C.M., Barrett B.,  
RT "Genome sequence of the human malaria parasite Plasmodium falciparum."  
RL Nature 419:498-511(2002).  
DR EMBL; AE014820; AAN36899.1; -.  
DR HSSP; P24295; 1AUP.  
DR GO; GO:0006520; P:amino acid metabolism; IEA.  
DR GO; GO:0006095; P:amino acid catabolism; IEA.  
DR InterPro; IPR006095; GLFV\_dehydrog.  
DR InterPro; IPR006096; GLFV\_dehydrog\_C.  
DR InterPro; IPR006097; GLFV\_dehydrog\_N.  
DR Pfam; PF02028; GLFV\_dehydrog; 1.  
DR Pfam; PF02812; GLFV\_dehydrog\_N; 1.

DR PRINTS; PR00082; GLFDHGRGNASE.  
DR PROSITE; PS00074; GLFV\_DEHYDROGENASE; 1.  
SQ SEQUENCE 510 AA; 5743 MW; AC400045297AC64P CRC64;

Query Match 55.8%; Score 1375; DB 2; Length 510;  
Best Local Similarity 60.0%; Pred. No. 2.7e-88;  
Matches 267; Conservative 66; Mismatches 104; Indels 8; Gaps 5;

QY 36 VRQLLTETPKDQEQEFMQAVREVAVLSQVFPKRPPELLIFIKQIIVPEPVTFRVSWL 95  
DB 70 IEELREKVYSKNKNEPEFLQAFEEVLSCLKDFVKDNYVIGVLENIAPERVIOPRVPMI 129

QY 96 DDAGNLQVNRFRVQYSSAIGPYKGLRPHPSVNLSTMKFLAEPQIFKNSLTTLPMGGGK 155  
DB 130 NDKEHKNRGRFRVQYNSVLGPYKGRPHPTVNLNVKIFLGFQIFKNSLTTLPMGGGK 189

QY 156 GGSDFDPKGSKDAEVMRFCQSFMTTELQRIHSYVQDVPAGDIGVAREIGYLFQYKRTIK 215  
DB 190 GGSDFDPKGSSENLKFCQSPMTNLFYIGPNTDVPAGDIGVAREIGYLFQYKRLKN 249

QY 216 NYTVLPKQOEGGSEIRPEATGYGAVLFVENVLKDGSLSKGRCLVSGAGNVAQYCA 275  
DB 250 SFEGVLTKGNIKWGGSNIRAEATGYGVYFAENVLKDNLNENKCKCLVSGSGNVAQYLV 309

QY 276 ELLLEKGAIVLSLSDSQYVYEPNGFTREQLQAVQDMKKNNNSARISEY--KSDTAVYV 333  
DB 310 EKLTEKGAIVLUTSDSGYIIEPNGFTREQLNYIMDI-KNNQRLRLKEYLKYSTAKYF- 367

QY 334 DRRKPWELDCQVDIAPPCATONEIDEHDAELLIKHGCGQVYVGGANPNSTNEAIHKYNKAG 393  
DB 368 ENQKPMWIPC--DIAPPCATONEINENDADLFQNKCKMIVEGANMPTHIKALHKLKQNN 425

QY 394 IICYCPGKAANAGGVAVSGLEMTQNRMSLNTWTRREVRDKLERIMKDIYDSAMGPSRRY--N 451  
DB 426 IILCPSKAANAGGVAVSGLEMSQNSMRLQWTHQETDMKLQIMKSIYEQCHNTSKIYLN 485

QY 452 VDLAAGANIAGFTKVDADAKQAGV 476  
DB 486 SDLVAGANIAGFLKVAADSFLQGG 510

RESULT 3  
Q7RQ39 PRELIMINARY; PRT; 1203 AA.

AC Q7RQ39;  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Glutamate dehydrogenase.  
GN Name=PY01264;  
OS Plasmodium yoelii yoelii.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=73239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=17XNL.  
RX PubMed=12368865; DOI=10.1038/nature01099;  
RA Carlton J.M., Angioli S.V., Suh B.B., Kooij T.W., Pertea M.,  
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,  
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.P., Bidwell S.L.,  
RA Shallow S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,  
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,  
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,  
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,  
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,  
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,  
RA Carucci D.J.  
RT "Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii."  
RL Nature 419:512-519(2002).  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.

EMBL; AABL01000331; EAA20557.1; --  
DR HSSP; P24295; 1AUP.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0006520; P:amino acid metabolism; IEA.  
DR InterPro; IPR006095; Exo endo phos.  
DR InterPro; IPR006096; GLFV dehydrog.  
DR InterPro; IPR006097; GLFV dehydrog\_N.  
DR Pfam; PF00372; Exo endo phos; 1.  
DR Pfam; PF00208; GLFV dehydrog; 1.  
DR PRINTS; PR00082; GLFV dehydrog N; 1.  
DR PROSITE; PS00074; GLFV DEHYDROGENASE; 1.  
SQ SEQUENCE 1203 AA; 13909 MW; DBE1988BD4C21715 CRC64;  
  
Query Match 55.2%; Score 1361; DB 2; Length 1203;  
Best Local Similarity 59.3%; Pred. No. 7.9e-97;  
Matches 264; Conservative 65; Mismatches 108; Indels 8; Gaps 5;  
  
QY 36 VRLQLTEIFPKDPEQEFMQAVREAVSLQPVFKRPELLPIPKQIVPEPVIPTFVSWL 95  
DB 763 IEMKENVISKNKDQHEFLQAFEVLTSLKPVFKNNIYLVLENISEPVIQFRVPI 822  
  
QY 96 DDAGNLQVNRGRFRVQYSSAIGPYKGLRFPSPVNLSTIMKFLAFQIPKNSLTTLPMGGG 155  
DB 823 NNGEHKINRGFRVQYSSVILGPYKGLRFPHTVNLSTVIRKPLGFEQIPKNSLTTLPMGGG 882  
  
QY 156 GGSDFDPKGSDAEVMRFQCSFMTLQRIHSYVDVPAGDIGVAREIGYLFQYKRIK 215  
DB 883 GGSDFDPKGSNEILRFQCSFMDNLFRIYGNPTDIPAGDIGVAREIGYLFQYKRLKN 942  
  
QY 216 NTGVLTPGQYGGSEIRPEATGYGAVLFVENLKDKGESLKGKRLVSGAGNVAQYCA 275  
DB 943 KFEGLTGKNIKWGSNNIRSEATGYGAVFAENALSDMNSLKNKTCTVSGSGNVAQYLV 1002  
  
QY 276 ELLLEKGAIVLSLSDSQYVYPNGFTREQLQAVQDMKKNSARISEY--KSDTAVYVG 333  
DB 1003 EKLIEKGAIVLTSDDSGYILEPNGFTKQLDIMEIKNVKRE-RIKEYLKYSKAKFF- 1060  
  
QY 334 DRKRPWELDCQVDIAPPCATQNEIDHDAELLIKHCQYVVEGANMPSNEAIHKYNKAG 393  
DB 1061 ENKPNWVFC--DIVPFCATQNEITENDADLLIKNCKLLVVEGANMPTHIKAWHKLKENK 1118  
  
QY 394 ILYCPKAAAGVAVSGLEMTQNRMSLNTWREVRDKLERIMKDIYDSAMGPSRRY--N 451  
DB 1119 ILICPSKAAAGVAVSGLEMSQNRMSLNTWREVRDKLERIMKDIYDSAMGPSRRY--N 451  
  
QY 452 VDLAAGANTAGTKVADAVKAQAV 476  
DB 1179 TDLVAGANTAGTKVADSVFIEQGL 1203

RESULT 4  
QY7YU9  
ID Q7YU9 PRELIMINARY; PRT; 446 AA.  
AC Q7YU9  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Glutamate dehydrogenase (fragment).  
GN Name=gdh;  
OS Spiroplasma barchanensis.  
OC Eukaryota; Diplomonadida; Hexamitidae; Hexamitinae; Spiroplasma.  
OX NCBI\_TaxID=103874;  
RN [1]  
RW SEQUENCE FROM N.A.  
RP STRAIN=ATCC 50380;  
RX PubMed=12820901; DOI=10.1186/1471-2148-3-14;  
RA Andersson J.O., Roger A.J.;  
RT "Evolution of glutamate dehydrogenase genes: evidence for lateral gene transfer within and between prokaryotes and eukaryotes.";  
RL BMC Evol. Biol. 3:14-14(2003).  
DR EMBL; AF533884; AAP83851.1; --

DR HSSP; P24295; 1AUP.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0006520; P:amino acid metabolism; IEA.  
DR InterPro; IPR006095; GLFV dehydrog.  
DR InterPro; IPR006096; GLFV dehydrog\_C.  
DR InterPro; IPR006097; GLFV dehydrog\_N.  
DR Pfam; PF00208; GLFV dehydrog; 1.  
DR Pfam; PF02812; GLFV dehydrog N; 1.  
DR PROSITE; PS00074; GLFV DEHYDROGENASE; 1.  
FT NON\_TER 1  
SQ SEQUENCE 446 AA; 49309 MW; AEB43D2A1762DB80 CRC64;  
  
Query Match 53.9%; Score 1328; DB 2; Length 446;  
Best Local Similarity 58.6%; Pred. No. 4.6e-85;  
Matches 262; Conservative 65; Mismatches 110; Indels 10; Gaps 6;  
  
QY 35 DVRLQLTEIFPKDPEQEFMQAVREAVSLQPVFKRPELLPIPKQIVPEPVIPTFVSW 94  
DB 5 DUKNVLQQ---RDANNIFCQAVNEIDSLTVFEEENPKYISVFQQLLEPERVIMFRVPM 61  
  
QY 95 LDDAGNLQVNRGRFRVQYSSAIGPYKGLRFPSPVNLSTIMKFLAFQIPKNSLTTLPMGGG 154  
DB 62 TDDKGEVAINRGYRVQYNSALGPYKGLRFPSPVNLSTIMKFLAFQIPKNSLTTLPMGGG 121  
  
QY 155 KGSDFDPKGSDAEVMRFQCSFMTLQRIHSYVDVPAGDIGVAREIGYLFQYKRIK 214  
DB 122 KGSDFDPKGSNGEVMRFQCSFMTLSRHHIQFTDVPAGDIGVAREIGYLFQYKRIK 181  
  
QY 215 KNYTGVLPQYGGSEIRPEATGYGAVLFVENLKDKGESLKGKRLVSGAGNVAQYCA 274  
DB 182 NOFTGILTKGAYSWGSLIRPEATGYGAVYVNLNEMMLDNGDDIKGRKLLSGAGNVAQFA 241  
  
QY 275 AELLLEKGAIVLSLSDSQYVYPNGFTREQLQAVQDMKKNSARISEY--KSDTAVYVG 332  
DB 242 TEKLHYGAIPLSLSDSNGTIEPNGFTAEQLKAWMDLKNIKR-GRLSYTSNSTAKY 300  
  
QY 333 GDRKRPWELDCQVDIAPPCATQNEIDHDAELLIKHCQYVVEGANMPSNEAIHKYNK 391  
DB 301 -EGQRPWAVYEGKVDVIMPCATQNEVNGTEAEARVILKGLRYVSEGANMPSNDIAHYHS 359  
  
QY 392 AGIYCPKAAAGVAVSGLEMTQNRMSLNTWREVRDKLERIMKDIYDSAMGPSRRY--N 451  
DB 360 SKVFGPKAAAGVAVSGLEMTQNRMSLNTWREVRDKLERIMKDIYDSAMGPSRRY--N 451  
  
QY 452 V--DLAAGANTAGTKVADAVKAQAV 476  
DB 420 KKNYQFGANVAGFLKVDASMDIDQCV 446

RESULT 5  
Q7R3N7  
ID Q7R3N7 PRELIMINARY; PRT; 449 AA.  
AC Q7R3N7  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE GLP 39 39379 38030.  
OS Giardia lamblia ATCC 50803.  
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.  
OX NCBI\_TaxID=184922;  
RN [1]  
RW SEQUENCE FROM N.A.  
RP STRAIN=WB C6;  
RA Morrison H.G.; McArthur A.G.; Adam R.D.; Aley S.B.; Gillin F.D.;  
RA Olsen G.J.; Sogin M.L.;  
RT "Draft sequence of the Giardia lamblia genome.";  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; AACB01000014; EAA41919.1; --  
DR HSSP; P24295; 1AUP.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.







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Db 360 AGILYAPGKASAGGAVATSGLEMSQNAIRLSWTREVDQRLFGIMQSHESCL-----KYG 415
QY 451 ----NVDLAAGANIAGFTKVAADAKAQQ 474
Db 416 KVGDTVNYVNGANIAGFVKVADAMLAQQ 443

RESULT 9
Q9UT56
ID Q9UT56 PRELIMINARY; PRT; 444 AA.
AC Q9UT56;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Glutamate dehydrogenase (EC 1.4.1.4).
GN Name=gdhA; OrderedLocNames=NMA1964;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=22491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagals K., Leather S., Moule S., Mungall K.L., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrett B.G.,
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis 22491."
RL Nature 404:502-506 (2000).
DR EMBL; AL162757; CAB85184.1; -.
DR PIR; B81825; B81825.
DR HSP; P24295; 1AUP.
DR GO; GO:0004354; F:glutamate dehydrogenase (NADP+) activity; IEA.
DR GO; GO:0016493; F:oxidoreductase activity; IEA.
DR GO; GO:0008520; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV dehydrog.
DR InterPro; IPR006096; GLFV dehydrog. C.
DR InterPro; IPR006097; GLFV dehydrog. N.
DR Pfam; PF02028; GLFV dehydrog. 1.
DR Pfam; PF02812; GLFV dehydrog. N; 1.
DR PRINTS; PR00082; GLFDHNRGNASE.
DR PROSITE; PS00074; GLFV DEHYDROGENASE; 1.
KW Complete proteome; Oxidoreductase.
SQ SEQUENCE 444 AA; 48462 MW; DE7F1A7B8DD6F424 CRC64;

Query Match 52.5%; Score 1294.5; DB 2; Length 444;
Best Local Similarity 57.1%; Pred. No. 1e-82;
Matches 256; Conservative 72; Mismatches 105; Indels 15; Gaps 6;

QY 35 DVRLTLTEFMKDPPQOEPMQAVREAVVSLQVPEKRELLP--PIPKQIVBERVITRV 92
Db 3 DLNTLFLANLKQRNPQEPHQAVVEVFNLSLDFLANPKYTOQSLELRIEVEPVRVNR 62

QY 93 SWLDDAGNLQVNRGRVQYSSAIGPYKGLRPHSPVNLISIMKFLAPEQIFKNSLTLP 152
Db 63 TWQDDKGQVQVNRGRVQYSSAIGPYKGLRPHSPVNLISIMKFLAPEQIFKNSLTLP 122

QY 153 GKGSDGDFPKGKSDAEVNRFCQSPMTLQRIHSYVQDVPAGDIGVAREIGYLFQYKR 212
Db 123 GKGSDGDFPKGKSDAEVNRFCQSPMTLQRIHSYVQDVPAGDIGVAREIGYLFQYKR 182

QY 213 IFTKNTTVGLTPKQEGYSGEIRPEATGYGAVLFVENVLKDGSGLKGRCLVSGAGNVAQ 272
Db 183 INNEPSSVLTKGLEWGLIIRPEATGYGCVVFAQAMLQTRNDSFEGKRVLSGSGNVAQ 242

QY 273 YCAELLLKGAIVLSLSDSQGYVYEP-NGFTREQVQAVQDMKKNSARISYKSDTAVY 331
Db 243 YAAEKAIQIGAKVLTVSDNSGFLVFPDSGMSQAQLAALITELKEVRRE-RVATYAEQGLQ 301

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QY 332 VDRKRKHELDCQVDIAPPCATQNEIDEDHDAELLIKHGCQYVVBGANPSTNEATHKYNK 391
Db 302 YFENQKPMGV--AAEIALPCATQNEIDEDHDAELLIKHGCQYVVBGANPSTIGAVEQRIK 359

QY 392 AGIYCPGKAANAGGAVSGLQEMTQNRMSLNTWTRREVRDKLERIMKDIYDSAMGPSRRY- 450
Db 360 AGILYAPGKASAGGAVATSGLEMSQNAIRLSWTREVDQRLFGIMQSHESCL-----KYG 415

QY 451 ----NVDLAAGANIAGFTKVAADAKAQQ 474
Db 416 KVGDTVNYVNGANIAGFVKVADAMLAQQ 443

RESULT 10
Q88Q23
ID Q88Q23 PRELIMINARY; PRT; 449 AA.
AC Q88Q23;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Glutamate dehydrogenase.
GN Name=gdhA; OrderedLocNames=PP0675;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22423060; PubMed=12534463;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
RA Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
RA Moazzes A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moezt D.,
RA Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
RA Kiewitz C., Eissen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440."
RL Environ. Microbiol. 4:799-808 (2002).
DR EMBL; AE016776; AAN66300.1; -.
DR HSP; P24295; 1AUP.
DR TIGR; PP0675; -.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV dehydrog.
DR InterPro; IPR006096; GLFV dehydrog. C.
DR InterPro; IPR006097; GLFV dehydrog. N.
DR Pfam; PF02028; GLFV dehydrog. 1.
DR Pfam; PF02812; GLFV dehydrog. N; 1.
DR PRINTS; PR00082; GLFDHNRGNASE.
DR PROSITE; PS00074; GLFV DEHYDROGENASE; 1.
KW Complete proteome.
SQ SEQUENCE 449 AA; 48871 MW; EF1733B6ABC89627 CRC64;

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Query Match 52.2%; Score 1287.5; DB 2; Length 449;
Best Local Similarity 58.2%; Pred. No. 3.3e-82;
Matches 259; Conservative 55; Mismatches 124; Indels 7; Gaps 4;

QY 36 VRLTLTEFMKDPPQOEPMQAVREAVVSLQVPEKRELLP--IFKQIVBERVITRV 93
Db 8 VDNFLARLKQDDPQEPHQAVVEVLTLPFLFANPHYLSGLERIVPERAVLFRVS 67

QY 94 WLDDAGNLQVNRGRVQYSSAIGPYKGLRPHSPVNLISIMKFLAPEQIFKNSLTLP 153
Db 68 WDDQKQVQVNRGRVQYSSAIGPYKGLRPHSPVNLISIMKFLAPEQIFKNSLTLP 127

QY 154 GKGSDGDFPKGKSDAEVNRFCQSPMTLQRIHSYVQDVPAGDIGVAREIGYLFQYKR 213
Db 128 GKGSDGDFPKGKSDAEVNRFCQSPMTLQRIHSYVQDVPAGDIGVAREIGYLFQYKR 187

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QY 214 TKNYTGVLTTPKQOBYGSGSIRPEATGYGAVLFVENVLKDGESLKGKRCCLVSGAGNVAQY 273  
 Db 188 ANOFTSVLTGKMTYGGSLRPEATGYGAVLFVENVLKDGESLKGKRCCLVSGAGNVAQY 247  
 QY 274 CAELLEKGAIVLSLSDSQYVYEPNGFTREQLQAVQDMKKKNSARISEYKSDTAVVVG 333  
 Db 248 AARKVNDLGGKVISLSDSEGTLYAAGLTDQWDLMLKXVXR-CRISLACQGFLEFR 306  
 QY 334 DRKPKWELDCQVDIAPPCATQNEIDEHDAELLIKHKGCQYVVEGANNPSTNEAIHKYNKAG 393  
 Db 307 KGQTPMSLPC--DIALPCATQNEBELGAEDARTLLRNGCICVAEGANNPTTLEAVDIFLDAG 364  
 QY 394 ILYCPCKAANAGVAVSGLEMTQNRMSLNTWREVRDKLERIMKOIYDSAM--GPERRYN 451  
 Db 365 ILYAPKASNAGVAVSGLEMSQNAWRLRLWTAGEVDSKLHNIMQSIHHACVHYGEADGR 424  
 QY 452 VDLAAGANTAGFTKVDADAKAQAQAV 476  
 Db 425 INYVKGANTAGFTKVDADAKAQAQAV 449

## RESULT 11

Q923C4 ID Q923C4 PRELIMINARY; PRT; 445 AA.  
 AC Q923C4; ID Q923C4; PRELIMINARY; PRT; 445 AA.  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE NADP-glutamate dehydrogenase (EC 1.4.1.4).  
 GN Name=gdh;  
 OS Pseudomonas aeruginosa.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=287;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PAC1;  
 RA Ansari F.;  
 RL Thesis (1994), University of London London U.K.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PAC1, and PAO1;  
 RA Brown P.R.;  
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PAO1;  
 RA Ansari F.;  
 RL Thesis (1994), University of London, London U.K.  
 DR EMBL; Y18494; CAA77192.1; -.  
 DR EMBL; Y15166; CAA75437.1; -.  
 DR HSSP; P24295; 1AUP.  
 DR GO; GO:0004354; F:glutamate dehydrogenase (NADP+) activity; IEA.  
 DR GO; GO:0016494; F:oxidoreductase activity; IEA.  
 DR GO; GO:0006520; P:amino acid metabolism; IEA.  
 DR GO; GO:0006095; G:glutamate dehydrogenase; IEA.  
 DR InterPro; IPR006095; GLFV dehydrog.  
 DR InterPro; IPR006095; GLFV dehydrog.  
 DR InterPro; IPR006095; GLFV dehydrog.  
 DR Pfam; PF0208; GLFV dehydrog\_N.  
 DR Pfam; PF0208; GLFV dehydrog\_N.  
 DR Pfam; PF0208; GLFV dehydrog\_N.  
 DR PRINTS; PS00082; GLFV dehydrog\_N.  
 DR PROSITE; PS00074; GLFV dehydrog\_N.  
 KW Oxidoreductase.  
 SQ SEQUENCE 445 AA; 48532 MW; B00DDE8E03A06D8A CRC64;

Query Match 52.1%; Score 1285; DB 2; Length 445;  
 Best Local Similarity 58.4%; Pred. No. 4.8e-82;  
 Matches 261; Conservative 56; Mismatches 118; Indels 12; Gaps 5;

QY 36 VRLQTEIFMKDPEQOEFMQAVREAVSLQPFVFEKRPPELLP--IFKQIVEPERVITFRVS 93  
 Db 5 VDAFLERLKRDPDQPEFHQAVEVLRLSLWPFLEANPHYLEAGIIRIIVEPERAILFRVP 64

QY 94 WLDDAGNTQVNRGFRVQYSSAIGPYKGLRPHPSVNLSTIMKFLAEQIFKNSLTTLPMGG 153  
 Db 65 WYDDQGRVRVNRGFRVQYSSAIGPYKGLRPHPSVNLSTIMKFLAEQIFKNSLTTLPMGG 124  
 QY 154 KGKGSDFOPKGSDAEVMRFQCSFMTLORHLSYVQDPVAGDIGVCAREIGVLFQGYKRI 213  
 Db 125 KGKGSDFOPKGSDAEVMRFQCSFMTLORHLSYVQDPVAGDIGVCAREIGVLFQGYKRI 184  
 QY 214 TKNYTGVLTTPKQOBYGSGSIRPEATGYGAVLFVENVLKDGESLKGKRCCLVSGAGNVAQY 273  
 Db 185 SNQFTSVLTGKLSYGGSLRPEATGYGAVLFVENVLKDGESLKGKRCCLVSGAGNVAQY 244  
 QY 274 CAELLEKGAIVLSLSDSQYVYEPNGFTREQLQAVQDMKKKNSARISEYKSDT---AV 330  
 Db 245 AARKVNDLGGKVISLSDSEGTLYAAGLTDQWDLMLKXVXR-CRISLACQGFLEFR 306  
 QY 331 YVDRRKWELDCQVDIAPPCATQNEIDEHDAELLIKHKGCQYVVEGANNPSTNEAIHKYN 390  
 Db 301 OFLEGVPPWGLAC--DIALPCATQNEBELGAEDARTLLRNGCICVAEGANNPTTLEAVDIFLDAG 364  
 QY 391 KAGIIPCPCKAANAGVAVSGLEMTQNRMSLNTWREVRDKLERIMKOIYDSAM--GPERRYN 451  
 Db 359 EAGIILYAPKASNAGVAVSGLEMSQNAWRLRLWTAGEVDSKLHNIMQSIHHACVHYGEADGR 424  
 QY 450 YNVDLAAGANTAGFTKVDADAKAQAQAV 476  
 Db 419 GRNVYVKGANTAGFTKVDADAKAQAQAV 445

## RESULT 12

Q7YZU7 ID Q7YZU7 PRELIMINARY; PRT; 437 AA.  
 AC Q7YZU7; ID Q7YZU7; PRELIMINARY; PRT; 437 AA.  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Glutamate dehydrogenase (Fragment).  
 GN Name=gdh;  
 OS Trichomonas vaginalis.  
 OC Eukaryota; Parabasalidea; Trichomonada; Trichomonadida;  
 OC Trichomonadidae; Trichomonadinae; Trichomonas.  
 OX NCBI\_TaxID=5722;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=12820901; DOI=10.1186/1471-2148-3-14;  
 RA Andersson J.O., Roger A.J.;  
 RT "Evolution of glutamate dehydrogenase genes: evidence for lateral gene transfer within and between prokaryotes and eukaryotes.";  
 RL BMC Evol. Biol. 3:14-14 (2003).  
 DR EMBL; AF533886; AAP83853.1; -.  
 DR HSSP; P24295; 1AUP.  
 DR GO; GO:0016494; F:oxidoreductase activity; IEA.  
 DR GO; GO:0006520; P:amino acid metabolism; IEA.  
 DR InterPro; IPR006095; GLFV dehydrog.  
 DR InterPro; IPR006095; GLFV dehydrog.  
 DR InterPro; IPR006095; GLFV dehydrog.  
 DR Pfam; PF0208; GLFV dehydrog\_N.  
 DR Pfam; PF0208; GLFV dehydrog\_N.  
 DR Pfam; PF0208; GLFV dehydrog\_N.  
 DR PROSITE; PS00074; GLFV dehydrog\_N.  
 FT NON TER 1  
 SQ SEQUENCE 437 AA; 47861 MW; 75205554DAFBF96 CRC64;

Query Match 52.1%; Score 1284.5; DB 2; Length 437;  
 Best Local Similarity 59.0%; Pred. No. 5.1e-82;  
 Matches 255; Conservative 56; Mismatches 118; Indels 3; Gaps 2;

QY 46 KDEQOEFMQAVREAVSLQPFVFEKRPPELLP--IFKQIVEPERVITFRVSWLDDAGNLQVNR 105  
 Db 4 RDPDQKEIFIQAVTEVLTSLVFILEKEPKYQKLLPALVEPERVIMFRVFNVDKGMWNR 63  
 QY 106 GFRVQYSSAIGPYKGLRPHPSVNLSTIMKFLAEQIFKNSLTTLPMGGKGSDFDPKKG 165  
 Db 64 GFRVQYSSAIGPYKGLRPHPSVNLSTIMKFLAEQIFKNSLTTLPMGGKGSDFDPKKG 123

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QY 166 SDAEVMRFQCSFWTELORHISYVDVPAGDIGVGAREIGYLFQGYKRITKNYTVGLTPKG 225
DB 124 SDGEVMRFQCSFWTELSRLSGTNDVPAGDIGVGAREIGYMFQGYKRITKNVFEGLTGGK 183
QY 226 QYGGSEIRPEATGAVGVFENVLKDGESLKGKCLVSGAGNVAQYCAELLLKGAIV 285
DB 184 ISFGSLIRPEATGVLGVFTVTEMLRAGEEIKGRAMVSGSNGVAQYCCQKLQIGALP 243
QY 286 LSLSDSQGYVYPNGFTREQLQAVQDMKK--KNSARISEYKSDTAVY--VGDRRKPWELD 342
DB 244 VSCSDSHGALIPKDGWTKHELDVNMHIKNVARTELKKISELPPDLKGYEIDKGSIWACE 303
QY 343 QCVDTAFPCATONEIDEHDAELLIKHGQYVVEGANMPSTNEAIHKYNKAGIYICPGKAA 402
DB 304 VPCDMLGPLCATQNEILPEHPVIMVNGVKVLLAEGANMPSTNETIELYMKENIYYGPGKAA 363
QY 403 NAGGVAVSLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPRRRYNDVLAAGANTAG 462
DB 364 NAGGVAVSLEMTQNSVRLANSSEKVDKLEIMHNIPEAHSASEQVGVPLYKGANLAG 423
QY 463 FTKVADAVKAQG 474
DB 424 FKRVADAMLAYG 435

RESULT 13
O96940
ID O96940 PRELIMINARY; PRT; 470 AA.
AC O96940;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Glutamate dehydrogenase (NADP+) (EC 1.4.1.4).
GN Names:GLUDH; Synonyms=GDH;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=99089647; PubMed=9874251;
RA Wagner J.T., Luedemann H., Faerber P.M., Lottspeich F.,
RA Krauth-Siegel R.L.;
RT "Glutamate dehydrogenase, the marker protein of Plasmodium falciparum.
RT Cloning, expression and characterization of the malarial enzyme.";
RL Eur. J. Biochem. 258:813-819(1998).
RN [2]
SEQUENCE FROM N.A.
RA Li L.H., Li M., Wu Y.S., Wang P.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y12927; CAA73390.1; -.
DR EMBL; AY040586; AAK77969.1; -.
DR HSSP; P24295; 1AUP.
DR GO; GO:004354; F:glutamate dehydrogenase (NADP+) activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV dehydrog.
DR InterPro; IPR006096; GLFV dehydrog. C.
DR InterPro; IPR006097; GLFV dehydrog. N.
DR Pfam; PF02028; GLFV dehydrog. 1.
DR Pfam; PF02812; GLFV dehydrog. N. 1.
DR PRINTS; PR00082; GLFV dehydrog. N.
DR PROSITE; PS00074; GLFV DEHYDROGENASE; 1.
KW Oxidoreductase.
SQ SEQUENCE 470 AA; 52546 MW; 50A37C23484C387A CRC64;

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Query Match 51.9%; Score 1279.5; DB 2; Length 470;
Best Local Similarity 55.6%; Pred. No. 1.3e-81;
Matches 264; Conservative 62; Mismatches 130; Indels 19; Gaps 7;

QY 5 TGDFTALQKAVQMAKYKAGTEGLVHGKINPDPVRLQLLITEIFMKDPEQEQFMQAVREVAVSL 64
DB 8 TGFVVLDK-----NASNYESLV-----DQEMNNVYRVKLPDPNQVEFLQAFHEILYSL 57

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QY 65 QPVFEKPELLPIKQIVPEPVLITRVSWLDDAGNLQVNRGFRVOYSSAIGPYKGLRF 124
DB 58 KPLFMEEPKYLPITITLSEPERAIQFRVCMWDDNGVQRKNRCFRVQVNSALGPYKGLRF 117
QY 125 HPSVNLSTMKELAPEQIFKNSLTTLPMGGGKGGSDFPKGSDAEVMRFQCSFWTELRQH 184
DB 118 HPSVNLSTVKEFLPEQIFKNSLTGLSMGGGKGGSDFPKGSDEILKFCQAFNNELVYH 177
QY 185 ISYVDVPAGDIGVGAREIGYLFQGYKRITKNYTVGLTPKGOEYGGSEIRPEATGYGAVL 244
DB 178 IGPCTDVPAGDIGVGAREIGYLYGYKKIVNSFGTLTGKNVKNWGGSNLRVEATGYGLVY 237
QY 245 FVENVLKDKGESLKGKCLVSGAGNVAQYCAELLLKGAIVLSLSDSQGYVVEGNPTRE 304
DB 238 FVLEVLISLNPVSKQTAVVSGGNVALYCVQKLLHLNVKVLTLSDSNGYVVEPNPFTHE 297
QY 305 QLOAVQDMKKKONNARSISEY--KSDTAVYVGDRRKPWELDCQVDIAFPACATONEIDEHDA 362
DB 298 NLEFLIDLKKE- KKRIRKEYLNHSTAKYF-PNEKPMGVPC--TLAFFCATQNEINLEDA 353
QY 363 ELLIKHGQYVVEGANMPSTNEAIHKYNKAGIYICPGKAAAGVAVSLEMTQNRMSLN 422
DB 354 KLLQKNGCILVGEAGANPSTVDALNLPKSNIIYCPSKAANAGGVATISGLEMSQNFQPSH 413
QY 423 WTRREVRDKLERIMKDIYDSAMGPRRRY--NVDLAAGANTAGFTKVADAVKAQG 474
DB 414 WTRETVDEKLEIMRNIFACSENALKYTKNKYDLQAGANTAGFLUKVAESYIEQG 468

RESULT 14
Q8ILTO
ID Q8ILTO PRELIMINARY; PRT; 470 AA.
AC Q8ILTO;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NADP-specific glutamate dehydrogenase.
GN ORFNames=PF14_0164;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.S., Nene V., Shallow J., Suh B., Peterson J., Angiuoli S.,
RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M., Fairhead A.H., Fraunholz M.J., Roos D.S., Vaizy S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Nature 419:498-511(2002).
DR EMBL; AB014818; AAN36776.1; -.
DR HSSP; P24295; 1AUP.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV dehydrog.
DR InterPro; IPR006096; GLFV dehydrog. C.
DR InterPro; IPR006097; GLFV dehydrog. N.
DR Pfam; PF02028; GLFV dehydrog. 1.
DR Pfam; PF02812; GLFV dehydrog. N. 1.
DR PRINTS; PR00082; GLFV dehydrog. N.
DR PROSITE; PS00074; GLFV DEHYDROGENASE; 1.
SQ SEQUENCE 470 AA; 52546 MW; 50A37C23484C387A CRC64;

Query Match 51.9%; Score 1279.5; DB 2; Length 470;
Best Local Similarity 55.6%; Pred. No. 1.3e-81;
Matches 264; Conservative 62; Mismatches 130; Indels 19; Gaps 7;

```

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QY 5 TGDFTALQKAVKQMATKAGTEGLVHGIKNPDRVQLLTETPMKDPEQOEPMQAVREAVSL 64
Db 8 TGRFVVLDK-----NASVYESIV-----DQEMNNVYERVMKLDPNQVEFLQAFHEILYSL 57
QY 65 QPVFEKRPELLPTFKOIVPEPVIPTFRVSWLDDAGNLQVNRGRFRVOYSSAIGPYKGLRF 124
Db 58 KFLFMEEPXYLPIETLSPEPAIQFRVCWLDGNGVQRKNRCFRVOYNALGPYKGLRF 117
QY 125 HPSVNLISIMKFLAFEQIFKNSLTTLPMGGKGSGDFDPKGSDAEVMRFQCSFMTLQRH 184
Db 118 HPSVNLISIVKFLGFEQIFKNSLTGLSMGGKGSGDFDPKGSNDNETLKFCQAFMNELYRH 177
QY 185 ISYVDVPAGDVGAGREIGYLFQYKRTIKYVTGVLTPKGOBYGGSSEIRPEATGYGAVL 244
Db 178 IGPCTDVPAGDVGAGREIGYLYGQYKTVNSFNGTLTKNVKGGSNLRVEATGYGLY 237
QY 245 FVENVLKDGESLKGKRLVSGAGNVAQYCAELILLEKGAIVLSLSDSQGYVVEPNQFTRE 304
Db 238 FVLEVLKSLNIPVEKQTAVVSGSNVALYCVQKLLHLNVKVLTLSDSNGYVVEPNQFTRE 297
QY 305 QLQAVQDMKKKNSARISEY--KSDTAVVVGDRRKPWELDCQVDIAFPQCATQNEIDEHDA 362
Db 298 NLEFLIDLKEE-KKGRILEYLNHSSSTAKYF-PNEKPGVPC--TLAAPPQCATQNEINLEDA 353
QY 363 ELLIKHGCOYVVEGANMPTNEAIIHKYNKAGIYICPGKAANAGGVAVSGLEMTQNRMSLN 422
Db 354 KLLQXNGCILVGEGANMPTVDALNLFKSNIIYCPSKAANAGGVAVSGLMSQNFQFSH 413
QY 423 WTREVRDKLERIMKDIYDSAMPSPRY---NVDLAAGANIAGFTKVADAVKAQG 474
Db 414 WTRETVDKLEIMRNIFIACSENALKYTKNKYDLQAGANIAGFLKVAESYIEQG 468
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RESULT 15

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Q9TXS8
ID Q9TXS8 PRELIMINARY; PRT; 442 AA.
AC Q9TXS8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Glutamate dehydrogenase.
GN Name=GDH;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RC STRAIN=FCQ 27;
RA Yuan P., Stewart T.S.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF098675; AAD11789.1; -.
DR HSSP; P24295; IAU.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV dehydrog.
DR InterPro; IPR006096; GLFV dehydrog_C.
DR InterPro; IPR006097; GLFV dehydrog_N.
DR Pfam; PF02028; GLFV dehydrog; 1.
DR Pfam; PF02812; GLFV dehydrog N; 1.
DR PRINTS; PR00082; GLFV dehydrogase.
DR PROSITE; PS00074; GLFV dehydrogenase; 1.
SQ SEQUENCE 442 AA; 49432 MW; 9D3F8AA679CCE4CC CRC64;
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Query Match 51.3%; Score 1265; DB 2; Length 442;
Best Local Similarity 58.8%; Pred. No. 1.2e-80;
Matches 258; Conservative 57; Mismatches 114; Indels 10; Gaps 6;

QY 42 EFMK-DPEQOEPMQAVREAVSLQPVFEKRPELLDIPKQIVEPVIITFRVSLDDAGN 100
Db 6 ERMKLDPNQVEFLQAFHEILYSLKPLFMEEPXYLPIETLSPEPAIQFRVCWLDNGV 65
QY 101 LQVNRGRFRVOYSSAIGPYKGLRFHPSVNLISIMKFLAFEQIFKNSLTTLPMGGKGSGDF 160
```

```
Db 66 QRKNRCFRVOYNALGPYKGLRFHPSVNLISIVKFLGFEQIFKNSLTGLSMGGKGSGDF 125
QY 161 DPKGSDAEVNRFCOSFMTLQRHISYVQDVPAGDIGVGAREIGYLFQYKRTIKYNTGV 220
Db 126 DPKGSDNETLKFCQAFMNELYRHIGLPGCTDVPAGDIGVGRQIGYLYGQYKIVNSFNGT 185
QY 221 LTPKGOBYGGSSEIRPEATGYGAVLFEVNLKDKGESLKGKRLVSGAGNVAQYCAELILLE 280
Db 186 LTGKNVKGGSNLRVEATGYGLVFEVLEVLKSLNIPVEKQTAVVSGSNVALYCVQKLLH 245
QY 281 KGAIIVLSLSDSQGYVVEPNQFTREQLQAVQDMKKKNSARISEY--KSDTAVVVGDRRKP 338
Db 246 LNVKVLTLSDSNGYVVEPNQFTRENLFLIDLKEE-KKGRILEYLNHSSSTAKYF-PNEK 303
QY 339 WELDCQVDIAFPQCATQNEIDEHDAELLIKHGCOYVVEGANMPTNEAIIHKYNKAGIYICP 398
Db 304 KGVPCC--TLAAPPQCATQNEINLEDAKLLKNGCILVGEGANMPTVDALNLFKSNIIYCP 361
QY 399 GKAANAGGVAVSGLEMTQNRMSLNWTRBEVRDKLERIMKDIYDSAMPSPRY---NVDLA 455
Db 362 SKAANAGGVAVSGLMSQNFQFSHWTRETVDKLEIMRNIFIACSENALKYTKNKYDLQ 421
QY 456 AGANIAGFTKVADAVKAQG 474
Db 422 AGANIAGFLKVAESYIEQG 440

Search completed: September 8, 2005, 02:43:31
Job time : 87.1641 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 8, 2005, 02:27:13 ; Search time 20.6536 Seconds  
(without alignments)  
2217.496 Million cell updates/sec

Title: US-10-627-886-26  
Perfect score: 2465  
Sequence: 1 MDATTGDTALQKAVQMAT.....GANIAGFTKVADVAKQAGV 476  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Query Match | Length | ID       | Description        |
|------------|--------|-------------|--------|----------|--------------------|
| 1          | 2444   | 99.1        | 523    | 1 S17949 | glutamate dehydrog |
| 2          | 1324.5 | 53.7        | 449    | 1 A42489 | glutamate dehydrog |
| 3          | 1309   | 53.1        | 445    | 2 H83072 | glutamate dehydrog |
| 4          | 1300.5 | 52.8        | 444    | 2 H81050 | glutamate dehydrog |
| 5          | 1294.5 | 52.5        | 444    | 2 B81825 | glutamate dehydrog |
| 6          | 1238   | 50.2        | 449    | 2 A64053 | glutamate dehydrog |
| 7          | 1214.5 | 49.3        | 444    | 2 T10487 | glutamate dehydrog |
| 8          | 1214   | 49.2        | 448    | 2 D98019 | glutamate dehydrog |
| 9          | 1212   | 49.2        | 448    | 2 H95151 | NADP-specific glut |
| 10         | 1210.5 | 49.1        | 458    | 2 E83912 | NADP-specific glut |
| 11         | 1205.5 | 48.9        | 424    | 2 E75362 | glutamate dehydrog |
| 12         | 1201   | 48.7        | 447    | 1 DEECEN | glutamate dehydrog |
| 13         | 1199   | 48.6        | 443    | 2 F96990 | NADP-specific glut |
| 14         | 1198   | 48.6        | 447    | 2 C90337 | NADP-specific glut |
| 15         | 1198   | 48.6        | 447    | 2 G85785 | NADP-specific glut |
| 16         | 1189.5 | 48.3        | 458    | 2 A11503 | NADP-specific glut |
| 17         | 1185   | 48.1        | 447    | 2 S32227 | glutamate dehydrog |
| 18         | 1182   | 48.0        | 447    | 1 A33504 | glutamate dehydrog |
| 19         | 1181   | 47.9        | 447    | 2 AF0710 | NADP-specific glut |
| 20         | 1180.5 | 47.9        | 458    | 2 A11144 | NADP-specific glut |
| 21         | 1153   | 46.8        | 447    | 2 AE0483 | glutamate dehydrog |
| 22         | 1150   | 46.7        | 448    | 2 D64567 | glutamate dehydrog |
| 23         | 1143   | 46.4        | 450    | 2 S22403 | glutamate dehydrog |
| 24         | 1142.5 | 46.3        | 448    | 2 B95277 | probable glutamate |
| 25         | 1139   | 46.2        | 448    | 2 F71862 | glutamate dehydrog |
| 26         | 1133.5 | 46.0        | 446    | 2 S06938 | glutamate dehydrog |
| 27         | 1121.5 | 45.5        | 454    | 1 DENCEN | glutamate dehydrog |
| 28         | 1115.5 | 45.3        | 459    | 1 S04904 | glutamate dehydrog |
| 29         | 1109   | 45.0        | 457    | 2 S63608 | glutamate dehydrog |

ALIGNMENTS

RESULT 1

S17949  
glutamate dehydrogenase (NADP) (EC 1.4.1.4) precursor - Chlorella sorokiniana (fragment)  
N:Alternate names: glutamic dehydrogenase; NADP-specific glutamate dehydrogenase  
C:Species: Chlorella sorokiniana  
C>Date: 30-Jun-1992 #sequence revision 23-Mar-1995 #text\_change 09-Jul-2004  
C:Accession: S17949; S17950; S19030  
R:Cock, J.M.; Kim, K.D.; Miller, P.W.; Hutson, R.G.; Schmidt, R.R.  
Plant Mol. Biol. 17, 1023-1044, 1991  
A:Title: A nuclear gene with many introns encoding ammonium-inducible chloroplastic NADP  
A:Reference number: S17949; MUID:92032762; PMID:1718478  
A:Accession: S17949  
A:Molecule type: DNA  
A:Residues: 1-523 <COC>  
A:Cross-references: UNIPROT:P28998; EMBL:X58831  
A:Accession: S17950  
A:Molecule type: mRNA  
A:Residues: 1-523 <COC2>  
A:Cross-references: EMBL:X58832; NID:g18272; PIDN:CAA41636.1; PID:g18273  
R:Schmidt, R.R.  
submitted to the EMBL Data Library, April 1991  
A:Reference number: S19030  
A:Accession: S19030  
A:Molecule type: DNA  
A:Residues: 1-219, 'LW', 222-523 <SCH>  
A:Cross-references: EMBL:X58831  
C:Genetics:  
A:Genome: nuclear  
A:Introns: 6/2; 29/1; 40/3; 56/3; 85/3; 127/3; 149/3; 175/1; 183/3; 211/1; 246/1; 272/2,  
C:Superfamily: glutamate dehydrogenase (NAD(P)+)  
C:Keywords: Chloroplast; hexamer; NADP; oxidoreductase  
F:202/Binding site: substrate (Lys) #status predicted

Query Match 99.1%; Score 2444; DB 1; Length 523;  
Best Local Similarity 99.2%; Pred. No. 1.2e-174;  
Matches 472; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

|    |     |   |     |
|----|-----|---|-----|
| QY | 1   | MDATTGDTALQKAVQMATKAGTEGLVHGINKNPVROLLTEIFMKDPEQEFMOAVREV     | 60  |
| DB | 48  | MDATTGDTALQKAVQMATKAGTEGLVHGINKNPVROLLTEIFMKDPEQEFMOAVREV     | 107 |
| QY | 61  | AVSLQPVFKPEKPELLPIFKQIPEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG | 120 |
| DB | 108 | AVSLQPVFKPEKPELLPIFKQIPEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG | 167 |
| QY | 121 | GLRFPSPVNLISIMKFLAEPQIFKNSLTTLPMGGGGKGSDFDPKSGSDAEVWRFCSFWTE  | 180 |
| DB | 168 | GLRFPSPVNLISIMKFLAEPQIFKNSLTTLPMGGGGKGSDFDPKSGSDAEVWRFCSFWTE  | 227 |
| QY | 181 | LQRHSIYQDVPAGDIGVAREIGYLFQGYKRITKNYTGVLTPKQEGYGGSEIRPEATGY    | 240 |
| DB | 228 | LQRHSIYQDVPAGDIGVAREIGYLFQGYKRITKNYTGVLTPKQEGYGGSEIRPEATGY    | 287 |

|    |        |      |     |   |        |                    |
|----|--------|------|-----|---|--------|--------------------|
| 30 | 1092   | 44.3 | 451 | 2 | T41492 | probable glutamate |
| 31 | 1067.5 | 43.3 | 459 | 2 | S17907 | glutamate dehydrog |
| 32 | 1037.5 | 42.1 | 454 | 1 | A25275 | glutamate dehydrog |
| 33 | 1022   | 41.5 | 457 | 2 | S51960 | glutamate dehydrog |
| 34 | 994.5  | 40.3 | 624 | 2 | B96556 | hypothetical proce |
| 35 | 579.5  | 23.5 | 416 | 2 | T45284 | glutamate dehydrog |
| 36 | 576.5  | 23.4 | 416 | 2 | G72305 | glutamate dehydrog |
| 37 | 552.5  | 22.4 | 421 | 2 | F83852 | glutamate dehydrog |
| 38 | 551    | 22.4 | 424 | 2 | A70055 | glutamate dehydrog |
| 39 | 545.5  | 22.1 | 426 | 2 | G69933 | glutamate dehydrog |
| 40 | 544.5  | 22.1 | 414 | 2 | G89862 | NAD-specific gluta |
| 41 | 536    | 21.7 | 372 | 2 | G84220 | glutamate dehydrog |
| 42 | 530    | 21.5 | 420 | 2 | D75176 | glutamate dehydrog |
| 43 | 529.5  | 21.5 | 430 | 2 | F83989 | glutamate dehydrog |
| 44 | 527.5  | 21.4 | 420 | 2 | F84142 | glutamate dehydrog |
| 45 | 527.5  | 21.4 | 421 | 2 | B81079 | glutamate dehydrog |

```
QY 241 GAVLFVENVLKDKGESLKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQYVYEPNG 300
Db 288 GAVLFVENVLKDKGESLKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQYVYEPNG 347
QY 301 FTREQLQAVQDMKKKNSARISEYKSDTAVVYGDRRKPWELDCQVDIAPPCATQNEIDRH 360
Db 348 FTREQLQAVQDMKKKNSARISEYKSDTAVVYGDRRKPWELDCQVDIAPPCATQNEIDRH 407
QY 361 DAELLIKHGCGQYVVEGANMPSTNEAIHKYNKAGIYCPCGAANAGGAVVSGLEMTQNRMS 420
Db 408 DAELLIKHGCGQYVVEGANMPSTNEAIHKYNKAGIYCPCGAANAGGAVVSGLEMTQNRMS 467
QY 421 LNWTRREVDKLERIMKDIYDSAMGPRSRYNVDLAAGANIAGFTKVADAVKAQGV 476
Db 468 LNWTRREVDKLERIMKDIYDSAMGPRSRYNVDLAAGANIAGFTKVADAVKAQGV 523

RESULT 2
A42489
Glutamate dehydrogenase (NADP) (EC 1.4.1.4) - Giardia lamblia
N:Alternate names: glutamic dehydrogenase; NADP-specific glutamate dehydrogenase
C:Species: Giardia lamblia
C>Date: 31-Dec-1993 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C:Accession: A42489
R:Yee, J.; Dennis, P.P.
J.:Biol. Chem. 267, 7539-7544, 1992
A:Title: Isolation and characterization of a NADP-dependent glutamate dehydrogenase gene
A:Note: sequence extracted from NCBI backbone (NCBIN:94071, NCBI:94074)
A:Reference number: A42489; MUID:92218410; PMID:1559991
A:Accession: A42489
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-449 <STO>
A:Cross-references: UNIPROT:P28724; GB:M84604; NID:gl59108; PIDN:AAA29155.1; PID:gl59109
A:Note: sequence extracted from NCBI backbone (NCBIN:94071, NCBI:94074)
C:Superfamily: glutamate dehydrogenase (NAD(P)+)
C:Keywords: NADP; oxidoreductase
F:125/Binding site: substrate (Lys) #status predicted

Query Match 53.7%; Score 1324.5; DB 1; Length 449;
Best Local Similarity 58.2%; Pred. No. 4e-91;
Matches 260; Conservative 67; Mismatches 111; Indels 9; Gaps 5;

QY 36 VRQLLTIEMKDPQEQEFMQAVREVAVSLQPVFEKRPPELLP--IFKQIVPERVITPRVSWL 95
Db 6 IEELAVIKQDGHMTEFQAEEVVDLSKVIFEREPKYIPFERKLEPERVILIFRPVPM 65
QY 96 DDAGNLQVNRGRFRVQYSSAIGPYKGLRPHPSVNLISIMKFLAFEQIFKNSLTTLPMGGGK 155
Db 66 DDAGRLNVNRGRFRVQYNSALGPYKGLRPHPSVNLISILKFLGFEQILKNSLTTLPMGGGK 125
QY 156 GGSDFDPKGSDAEVMRFQCSFMTLQRLHISYVDVPAGDIGVGBAREIGYLPQGYKRTK 215
Db 126 GGSDFDPKGSDEVMRFQCSFMTLQRLHISYVDVPAGDIGVGBAREIGYLPQGYKRLRN 185
QY 216 NVTGVLTPKQBGVSGSEIRPEATGAVLFVENVLKDKGESLKRCLVSGAGNVAQYCA 275
Db 186 EFTGVLTKNVKMGSGSFIRPEATGAVLFVLEEMCKDNNTVIRGNVLSSGSGNVAQFAC 245
QY 276 ELLEKGAIVLSLSDSQYVYEPNGFTREQLQAVQDMKKKNSARISEYKS---DTAVV 332
Db 246 EKLIQLGAKVLTFSDSNGTIVDKGFNEBKLAHLMLKNEKR-GRVSEFKDKYPSVAYYE 304
QY 333 GDRRKPEW-LDCQVDIAPPCATQNEIDEHDAELLIKHGCGQYVVEGANMPSTNEAIHKYNK 391
Db 305 G--KKPWEFCQEQMPCIMPCATQNEVSGDDATRLVGLGLKFVAEGANMPSTAEAVHVYHA 362
QY 392 AGIIPCCKAANAGGAVVSGLEMTQNRMSLNMTREVRDKLERIMKDIYDSAMGPRSRYN 451
Db 363 KGVWGPAPKASNAGGVSUGLEMSQNSVRLQWTAEEVDQKLRGIRGIFVACRDATKAY 422
QY 452 --VDLAAGANIAGFTKVADAVKAQGV 476
Db 423 HPKNYQMGANIAGFLKVDMSIEQGCY 449
```

RESULT 3  
H83072

```
Glutamate dehydrogenase PA4588 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: H83072
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
gen
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: H83072
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-445 <STO>
A:Cross-references: UNIPROT:Q9HVJ7; GB:AE004872; GB:AE004091; NID:g9950829; PIDM:AG0797
A:Experimental source: strain PA01
C:Genetics:
C:Superfamily: glutamate dehydrogenase (NAD(P)+)
```

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Query Match 53.1%; Score 1309; DB 2; Length 445;
Best Local Similarity 59.2%; Pred. No. 5.7e-90;
Matches 263; Conservative 55; Mismatches 120; Indels 6; Gaps 4;
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```
QY 36 VRQLLTIEMKDPQEQEFMQAVREVAVSLQPVFEKRPPELLP--IFKQIVPERVITPRVS 93
Db 5 VDAFLERLKRDDPDQEPHQAVVEVLSLWFLFLEAPHYLEAGIIEIVEPERAILFRVP 64
QY 94 WLDDAGNLQVNRGRFRVQYSSAIGPYKGLRPHPSVNLISIMKFLAFEQIFKNSLTTLPMGG 153
Db 65 WVDDQGRVRVNRGVRVQMSAIGPYKGLRPHPSVNLISIMKFLAFEQIFKNSLTTLPMGG 124
QY 154 GKGSDPDPKGSDAEVMRFQCSFMTLQRLHISYVDVPAGDIGVGBAREIGYLPQGYKRI 213
Db 125 GKGSDPDPKGSDAEVMRFQCSFMTLQRLHISYVDVPAGDIGVGBAREIGYLPQGYKRL 184
QY 214 TKNYTVLTPKQBGVSGSEIRPEATGAVLFVENVLKDKGESLKRCLVSGAGNVAQY 273
Db 185 SNQFTSVLTGKLSYSGSLIRPEATGCGVFAQEMLKDRGDFDQGVVAISGSGNVAQY 244
QY 274 CABELLEKGAIVLSLSDSQYVYEPNGFTREQLQAVQDMKKKNSARISEYKSDTAVVYG 333
Db 245 AARKVMEMGGKVISLSDSBEGTLVABAGLSDSQWEYLMELKNVRR-GRIREMAEQPSLQFL 303
QY 334 DRRKPEWLDCCQVDIAPPCATQNEIDEHDAELLIKHGCGQYVVEGANMPSTNEAIHKYNKAG 393
Db 304 EGRRPWGLAC--DIALPCATQNEIDAEARLLANGCVCVAEGANMPSTLEAVDLFLEAG 361
QY 394 IIPCCKAANAGGAVVSGLEMTQNRMSLNMTREVRDKLERIMKDIYDSA-MGPSRRYV 452
Db 362 ILVAPGKASNAGGAVVSGLEMSQNSAMRLRWSEGEVDYTKLHGIMQSIHACILLYGEEQGV 421
QY 453 DLAAAGANIAGFTKVADAVKAQGV 476
Db 422 NVYKGANIAGFPVKVADAMLAQGV 445
```

RESULT 4  
H81050

```
Glutamate dehydrogenase, NADP-specific NMB1710 [imported] - Neisseria meningitidis (stra
in)
C:Species: Neisseria meningitidis
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: H81050
R:Tetelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.;
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain NC58.
```



[illegible]

Db 191 ACVFTGRLSPGSLIRPEATGYGLIYFAQMALEKGDSPAGKVYVSGSGNVAQYATK 250  
QY 278 LLEKGAIVLSLSDSGYVYEPNGFTTRBQLQAVODMKKGNNSARISEYKSDTAVYVGDRRK 337  
Db 251 ALSLAGKVVTCSDSGYVYDPNGFTTEKLAALFDI-KNTKRGKVDYAEQFGLQVPEGRK 309  
QY 338 PHELDQVDDIAPCATQNEIDEHDAELLIKHCQYVVEGANMPSINEAIHKYNKAGIYIC 397  
Db 310 PHEV--QVDIALPFCATQNELEISDQAORLIKNGVKLVAGANMPTTIEATEALLAADVLFG 367  
QY 398 PGKAANAGGAVVSGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRY----- 450  
Db 368 PGKAANAGGAVVSGLEMASSQRLYWTAAEVDQAHLRIMLDIHANC-----KKYGTIEQOE 423  
QY 451 NVDLAAGANIAGFTKVADAVKAQ 474  
Db 424 NINVVGVANVAGVFKVADAMLAQ 447

## RESULT 7

T10487  
glutamate dehydrogenase (NADP) (EC 1.4.1.4) - Prevotella ruminicola  
C:Species: Prevotella ruminicola  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C:Accession: T10487  
R:Wen, Z.T.; Morrison, M.  
submitted to the EMBL Data Library, December 1996  
A:Reference number: Z17049  
A:Accession: T10487  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Note: gdhA  
A:Cross-references: UNIPROT:P95544; EMBL:U82240; NID:g1772844; PID:g1772845  
A:Experimental source: strain B14  
C:Genetics:  
A:Superfamily: glutamate dehydrogenase (NAD(P)+)  
C:Keywords: NADP; oxidoreductase

Query Match 49.3%; Score 1214.5; DB 2; Length 444;  
Best Local Similarity 54.9%; Pred. No. 6.5e-83;  
Matches 242; Conservative 73; Mismatches 119; Indels 7; Gaps 4;  
QY 38 QLLTEIFMKDPQOEPMQAVREAVLSQVPEKRPDL--LPFKQIVPEPVRVITPRVSWL 95  
Db 5 EVIEKLKAKFPQGPYIQAQSVLGTIEBEYKNHPEFEKANLIERLCVDRILQFRVSWV 64  
QY 96 DDAGNLQVNRGPRVQYSSAIGPYKGLRPHSPVNLISIMKFLAPEQIFKNSLTTLPMGGSK 155  
Db 65 DNGNVQTNLGRVQNNNAIGPYKGLRPHKSVNASILKFLAFQTFKNSLTTLPMGGAK 124  
QY 156 GGSDFDPKGSDAEVMRFQCSFMTLQRIHSYVDVPAGDIGVGAREIGYLFQYKRIYK 215  
Db 125 GGSDFDPKGSDEVMRFQCFAMNELYRLIGPDEDVPAGDIGVGREGVYMGFYKLLTH 184  
QY 216 NYTGVLTTPKQBYGSGSEIRPEATGCAVLFVENVLKDGESLKGKRCIVSGAGNVAQYCA 275  
Db 185 QPGGILTGKLEFGGSLIRPEATGYNVYFLEDMLKTRGESLEGKTVLVSGSGNVAQYTI 244  
QY 276 ELLLEKGAIVLSLSDSGYVYEPNGFTTRBQLQAVODMKKGNNSARISEYKSDTAVVGD 335  
Db 245 EXKLQLGAKPVTCSDSNGYIYDPGIDAELKAFIMELKNVVR-GRIKEAYEKYGVYEN 303  
QY 336 RXPWELDCQVDIAFPATQNEIDEHDAELLIKHCQYVVEGANMPSINEAIHKYNKAGII 395  
Db 304 ARPW--GEKADIATPCATQNEINEABAKTLIANGVPAVSEGANMPTPEAAIKVFQDAKIL 361  
QY 396 YCPGKAANAGGAVVSGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAM--GPSRRYND 453  
Db 362 YCPGKASNAGGAVVATSGLEMSQNSRLSWTRREVDTKLHINIMDEIHANCYKGTPEPDGIN 421  
QY 454 LAAGANIAGFTKVADAVKAQ 474

Db 422 YVKGANVAGFMKVAKAMMAQ 442  
RESULT 8  
D98019  
glutamate dehydrogenase (NADP) (EC 1.4.1.4) [imported] - Streptococcus pneumoniae (strain  
C:Species: Streptococcus pneumoniae  
C:Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 09-Jul-2004  
C:Accession: D98019  
R:Hoekings, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burtgett, S.; DeHoff, B.S.; E.  
y, P.; Sun, P.M.; Winkler, M.E.  
J. Bacteriol. 183, 5709-5717, 2001  
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaekunas, S.R.;  
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
A:Reference number: A97872; MUID:21429245; PMID:11544234  
A:Accession: D98019  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-448 <KUR>  
A:Cross-references: UNIPROT:Q8DFG0; GB:AE007317; PIDN:AAK99984.1; PID:g15458813; GSPDB:G  
C:Genetics:  
A:Gene: gdhA  
C:Superfamily: glutamate dehydrogenase (NAD(P)+)  
C:Keywords: oxidoreductase  
Query Match 49.2%; Score 1214; DB 2; Length 448;  
Best Local Similarity 55.7%; Pred. No. 7.1e-83;  
Matches 248; Conservative 62; Mismatches 127; Indels 8; Gaps 4;  
QY 36 VRQLTEIFMKDPQOEPMQAVREAVLSQVPEKRPDL--LPFKQIVPEPVRVITPRV 93  
Db 8 IQSVFTVKARNGHEAEFLQAEFFNTLEVPFKHPEYIEENILARITEPERVISRPV 67  
QY 94 WLDDAGNLQVNRGPRVQYSSAIGPYKGLRPHSPVNLISIMKFLAPEQIFKNSLTTLPMGG 153  
Db 68 WDRDGKQVNRGPRVQYSSAIGPYKGLRPHSPVNLISIMKFLAPEQIFKNSLTTLPMGG 127  
QY 154 GKGSDFPKGSDAEVMRFQCSFMTLQRIHSYVDVPAGDIGVGAREIGYLFQYKRI 213  
Db 128 GKGSDFPKGSDEVMRFQCSFMTLQRIHSYVDVPAGDIGVGAREIGYLFQYKRI 187  
QY 214 TKNYTVLTTPKQBYGSGSEIRPEATGCAVLFVENVLKDGESLKGKRCIVSGAGNVAQY 273  
Db 188 NQFDAGVLTGKLEFGGSLIRPEATGYNVYFLEDMLKTRGESLEGKTVLVSGSGNVAQY 247  
QY 274 CAELLEKGAIVLSLSDSGYVYEPNGFTTRBQLQAVODMKKGNNSARISEYKSDTAVVVG 333  
Db 248 ALQKATELGATVIVSVDNSGVVIDENGI---DPDLLVDVKEKR-ARLTETAAEKATATY 303  
QY 334 DRRKPWELDCQVDIAFPATQNEIDEHDAELLIKHCQYVVEGANMPSINEAIHKYNKAG 393  
Db 304 HEGSVTVAGNYDIALPCATQNEINEABAKTLIANGVPAVSEGANMPSNDAIKVYKENG 363  
QY 394 ILYCPGKAANAGGAVVSGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRYV- 452  
Db 364 IFYCPKAANAGGAVVSALEMSQNSRLSWTRREVDGRLKDIIMTNIFNTAKTTSETYGLD 423  
QY 453 -DLAAGANIAGFTKVADAVKAQ 476  
Db 424 KDYLAGANIAFENVANMIAQGI 448

## RESULT 9

H95151  
NADP-specific glutamate dehydrogenase [imported] - Streptococcus pneumoniae (strain TIGR  
C:Species: Streptococcus pneumoniae  
C:Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 09-Jul-2004  
C:Accession: H95151  
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid  
on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,  
nson, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001





Ddb 300 TEGCDGHWKUC--DIALPCATQNEIDENSAKTILANGCVAVGGANMPSTIEAIVDLFIK 357

Qy 392 AGIYCPGAANAGGVASGLEMTQNRMSLNWTREVRDKLERIMKDIIYSAMGPSRRYN 451  
kv:| | | | | | | | : | | | | | : | | | | :

Ddb 358 NKVIFGPAKANAGGVATSALMSQNSMRYSWTFEEVDTKLQNTMKNIYIKCSNAANEYG 417  
: | | | | | | | | : | | | | | : | | | | :

Qy 452 VD--LAAGANIAGTFTKVADAVKAQG 474  
: | | | | | | | | : | | | | | : | | | | :

Ddb 418 FEDNLVAGANIAGTFTKVAEAMYSLG 442

RESULT 14

C90937 NAD<sup>+</sup>-specific glutamate dehydrogenase [imported] - Escherichia coli (strain O157:H7, sub C); Species: Escherichia coli

C; Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004

C; Accession: C90937

R; Hayaashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001

A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and generation of reference strains from cattle and sheep

A; Reference number: A9629; UID:21156231; PMID:11258796

A; Accession: C90937

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-447 <HAY>

A; Cross-references: UNIPROT:Q8XDW9; GB:BA000007; PIDN:BAB35890.1; PID:g13361934; GSPDB:G000000000

A; Experimental source: strain O157:H7, substrain RMD 0509952

C; Geneticks:

A; Gene: Ec62467

C; Superfamily: glutamate dehydrogenase (NAD(P)+)

| Query Match           | 48.6% | Score 1198  | DB 2           | Length 447 |
|-----------------------|-------|---|----------------|------------|
| Best Local Similarity | 53.8% | Pred. No. 1.1e-81   |                |            |
| Matches               | 240   | Conservative 68   | Mismatches 128 | Indels 10  |
| Gaps                  | 5     |   |                |            |
| QY                    | 36    | VRQLLTETFMKDPQOEFMQAVREVAVSLOPVEKPEL--LPFPQOIVEPERVITFRVS     | 93             |            |
| DB                    | 7     | LESFLNHVQKRDNQTEFAQAVREVTMTLPPFLQONPKYRQMSLLERLVEPERVIQFRVV   | 66             |            |
| QY                    | 94    | WLDDAGNLQVNRFRVQYSSAIGPYKGLRPHSPSVNLISIMKFLAFQEIFKNSLTTLLPMGG | 153            |            |
| DB                    | 67    | WVDDRQVQVNRARVQFSSAIGPYKGGMRPHSPSVNLISILKFLGFQTFKNAITLTLPMGG  | 126            |            |
| QY                    | 154   | KGGSDFDPKKGSDAEVMRFQSQFMTLEQRHISYVQDVPAGDIGVAREIGYLFQGVKRI    | 213            |            |
| DB                    | 127   | KGGSDFDPKKGSEGEVMRFQCALMTLXYRLHGADTDVPAGDIGVGREVGFPAGMMKKL    | 186            |            |
| QY                    | 214   | TKNYTGLVLPKGOEYGGSEIRPBATGYGAVLFVENVLKKGESLKGKRCILVSGAGNVAQY  | 273            |            |
| DB                    | 187   | SNNTACVFTKGKLSFGSLLIRPBATGYGLVYFTEAMLKRHGMGFEGMRVSVSGSNVAQY   | 246            |            |
| QY                    | 274   | CAELLEKGAIVLSLSDSQGVYEPNGFTTEQIQAVQDMKKKNSARISEYKSDTAVYVG     | 333            |            |
| DB                    | 247   | AIEKAMEFGARVITASDSSGVVDSGGFTTEKELARLEI--KSSRDGRVADYAKEFGLVYL  | 305            |            |
| QY                    | 334   | DREKPELDCQVDIAFPATQNEIDSHDABELLKHGCOYVVEGANMPTNEATHKNKAG      | 393            |            |
| DB                    | 306   | EGQOPHSV--PVDIALPCATQNELDVDAHQLTANGVKAVAEGANMPTTIEATLFPQAG    | 363            |            |
| QY                    | 394   | IIYCPGKAANAGGVAVSGLEMTQNRMSLNWTRBEVRDKLERIMKDIYDSAM---GPSRRY  | 450            |            |
| DB                    | 364   | VLFPAGKKAANAGGVATSGLEMAQNAARLGMKAKEKVDARLHHIMLDIHHCVEHGGEQRT  | 423            |            |
| QY                    | 451   | NVDLAAGANTAGTFTKVADAVKAQAV                                    | 476            |            |
| DB                    | 424   | N--YVGCANTAGTFTKVADAMLAQCVI                                   | 447            |            |

RESULT 15  
G85785  
NADP-specific glutamate dehydrogenase [imported] - Escherichia coli (strain O157:H7, sub  
C; Species: Escherichia coli

C; Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
C; Accession: G85785  
R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose,  
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoumis,  
Nature 409, 529-533, 2001  
A; title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.  
A; Reference number: A85480; MUID:21074935; PMID:11206551  
A; Accession: G85785  
A; Status: preliminary  
A; Molecule type: DNA  
A; Residues: 1-447 <STO>  
A; Cross-references: UNIPROT:Q8XDW9; GB:AE005174; NID:G12515786; PIDN:AAG566  
A; Experimental source: strain O157:H7, substrain EDL933  
C; Genetics:  
A; Gene: gdhA  
C; Superfamily: glutamate dehydrogenase (NAD(P) +)

| Query Match           | 48.6%; | Score 1198;  | DB 2; | Length 447;                       |
|-----------------------|--------|--|-------|-----------------------------------|
| Best Local Similarity | 53.8%; | Pred. No. 1.1e-81;   |       |                                   |
| Matches               | 240;   | Conservative   | 68;   | Mismatches 128; Indels 10; Gaps 5 |
| Qy                    | 36     | VRLLTEIFMKDPEQBFMQAVREVAUSLPQVFKRPEL--LPFQKQIIVERVITFRVS       | 93    |                                   |
|                       | :      |  |       |                                   |
| Db                    | 7      | LESFLNHVKRDPNQTEFAQAVREVMTTLPFFLEQNPQKRYQMSLLERLVEPERVITQFRV   | 66    |                                   |
|                       | :      |  |       |                                   |
| Qy                    | 94     | WLDDAGNLVNRCFRVQYSSAIGPYKGLSPHPSVNLISIMKFLAPEQIFKNSLITLPMGG    | 153   |                                   |
|                       | :      |  |       |                                   |
| Db                    | 67     | WDDRNQOVQNRARVQFSSAIGPYKGMGFPHPSVNLISILKFLGFQETFKNALTTPLPMGG   | 126   |                                   |
|                       | :      |  |       |                                   |
| Qy                    | 154    | KGKGSDFDPKKGSDAEVNRFCQGFMTLORHISVYQDVPAGDIGVGAREIGYLFQYKRI     | 213   |                                   |
|                       | :      |  |       |                                   |
| Db                    | 127    | KGKGSDFDPKKGSEGEVNRFCQALMTLYLRYHLGADTVDPAGDIGVGREVGFMAGMMKL    | 186   |                                   |
|                       | :      |  |       |                                   |
| Qy                    | 214    | TKNYTVGLTPKGOEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGRCLVSGAGNVAQY    | 273   |                                   |
|                       | :      |  |       |                                   |
| Db                    | 187    | SNNTACVFTKGSLPGGSLIRPEATGYGLVVFTEAMLKRHGMGEGMRVSVSGSGNVAQY     | 246   |                                   |
|                       | :      |  |       |                                   |
| Qy                    | 274    | CABLLLEKGAIVLSLSDSQGYVPEPNCFTREQLQAVQDMKKNNARSARISEYKSDTAVYVG  | 333   |                                   |
|                       | :      |  |       |                                   |
| Db                    | 247    | ALBKAMEFGARVITASDSSGTVYVDSGFTREKRLARLIEI-KSSRDGRVADYAKGFLGYVL  | 305   |                                   |
|                       | :      |  |       |                                   |
| Qy                    | 334    | DRKPKWELDCQVDIAPPCATQNEIDEHDAELLKHGCGQYVVEGANNMSTNEAIIHKYNKAG  | 393   |                                   |
|                       | :      |  |       |                                   |
| Db                    | 306    | EGQQPMSV--PVDIALPCATQNELVDAAHQLTANGVKAEGAEGANNMPTTEATELFOQAG   | 363   |                                   |
|                       | :      |  |       |                                   |
| Qy                    | 394    | IIYCPGKAANAGGAVVSGVLEMTQNRMSLNWTRBEVRDKLERIMKDLYDSAM---GPSRIR  | 450   |                                   |
|                       | :      |  |       |                                   |
| Db                    | 364    | VLFPAPGKAANAGGAVTSGLEMAQNAARLGHWAKEKYDARLHHMLIDIIHACVHEHGEQEQT | 423   |                                   |
|                       | :      |  |       |                                   |
| Qy                    | 451    | NVDLAAGANIAGTFKKVADAVKAQGA                                     | 476   |                                   |
|                       | :      |  |       |                                   |
| Db                    | 424    | N--YVOGANIAGPVKKVADAMLQGV                                      | 447   |                                   |
|                       | :      |  |       |                                   |

Search completed: September 8, 2005, 02:44:39  
Job time : 21.6536 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 8, 2005, 02:10:02 ; Search time 93.9092 Seconds  
(without alignments)  
1960.383 Million cell updates/sec

Title: US-10-627-886-26

Perfect score: 2465

Sequence: 1 MDATTGDTALQAKVQMAT.....GANIAGFTKVDVAKQAGV 476

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003s:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID | Description        |
|------------|--------|-------------|--------|-------|--------------------|
| 1          | 2465   | 100.0       | 476    | 2     | AAW15412 NADP-spec |
| 2          | 2465   | 100.0       | 476    | 5     | Aau98955 Mature NA |
| 3          | 2465   | 100.0       | 476    | 8     | Adq36731 Mature NA |
| 4          | 2465   | 100.0       | 487    | 5     | Aau98954 Mature NA |
| 5          | 2465   | 100.0       | 487    | 8     | Adq36729 Mature NA |
| 6          | 2465   | 100.0       | 512    | 2     | AAW15408 NADP-spec |
| 7          | 2465   | 100.0       | 512    | 5     | Aau98951 NADP-glut |
| 8          | 2465   | 100.0       | 512    | 8     | Adq36709 NADP-spec |
| 9          | 2465   | 100.0       | 526    | 5     | AAW15407 NADP-spec |
| 10         | 2465   | 100.0       | 526    | 8     | Aau98950 NADP-glut |
| 11         | 2465   | 100.0       | 526    | 8     | Adq36707 NADP-spec |
| 12         | 2457   | 99.7        | 445    | 2     | AAW15411 NADP-spec |
| 13         | 1309   | 53.1        | 445    | 6     | ABU38763 Protein e |
| 14         | 1309   | 53.1        | 450    | 7     | ABO71900 Pseudomon |
| 15         | 1300.5 | 52.8        | 444    | 8     | Adp08330 Neisseria |
| 16         | 1297.5 | 52.6        | 444    | 6     | ABP77942 N. gonorr |
| 17         | 1297.5 | 52.6        | 444    | 6     | ABU37205 Protein e |
| 18         | 1294.5 | 52.5        | 444    | 5     | Aau72986 Neisseria |
| 19         | 1294.5 | 52.5        | 444    | 6     | ABU38117 Protein e |
| 20         | 1287.5 | 52.2        | 449    | 6     | ABU39614 Protein e |
| 21         | 1281   | 52.0        | 445    | 8     | AdS24914 Bacterial |
| 22         | 1259   | 51.1        | 454    | 8     | Adn27186 Bacterial |
| 23         | 1257.5 | 51.0        | 462    | 6     | ABU17276 Protein e |
| 24         | 1257.5 | 51.0        | 467    | 6     | AdA34438 Acinetoba |
| 25         | 1250.5 | 50.7        | 448    | 5     | ABP65630 Bifidobac |

|    |        |      |     |   |                    |
|----|--------|------|-----|---|--------------------|
| 26 | 1239.5 | 50.3 | 448 | 6 | ABU29386 Protein e |
| 27 | 1239.5 | 50.3 | 448 | 8 | ADH97147 E. faecal |
| 28 | 1239   | 50.3 | 449 | 5 | Aau91467 Haemophil |
| 29 | 1238   | 50.2 | 449 | 4 | AAB88536 Haemophil |
| 30 | 1238   | 50.2 | 449 | 6 | ABU30172 Protein e |
| 31 | 1236.5 | 50.2 | 449 | 5 | ABP28423 Streptoco |
| 32 | 1234.5 | 50.1 | 448 | 7 | ADH85999 Enterococ |
| 33 | 1230.5 | 49.9 | 449 | 6 | ABU44405 Protein e |
| 34 | 1230   | 49.9 | 449 | 6 | ABU38946 Protein e |
| 35 | 1221   | 49.5 | 448 | 8 | ADK47974 Streptoco |
| 36 | 1214   | 49.2 | 448 | 6 | ABU46100 Protein e |
| 37 | 1212   | 49.2 | 448 | 6 | ABU01740 S. pneumo |
| 38 | 1211.5 | 49.1 | 448 | 8 | ADH97149 E. faecal |
| 39 | 1210.5 | 49.1 | 458 | 8 | ADS28251 Bacterial |
| 40 | 1207.5 | 49.0 | 464 | 6 | ABU23354 Protein e |
| 41 | 1205.5 | 48.9 | 424 | 8 | ADN17964 Bacterial |
| 42 | 1205.5 | 48.9 | 444 | 6 | ABU20518 Protein e |
| 43 | 1204   | 48.8 | 447 | 2 | AAW08092 Glutamina |
| 44 | 1201   | 48.7 | 447 | 2 | AAW60830 E. coli g |
| 45 | 1201   | 48.7 | 447 | 6 | ABU15360 Protein e |

#### ALIGNMENTS

##### RESULT 1

AAW15412

ID AAW15412 standard; protein; 476 AA.

AC AAW15412;

DT 17-OCT-2003 (revised)

DT 10-JUL-1997 (first entry)

DE NADP-specific glutamate dehydrogenase beta subunit.

KW Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;

KW chloroplast; transgenic plant.

OS Chlorella sorokiniana; strain UTEX 1230.

PN WO9712983-Al.

PD 10-APR-1997.

PF 03-OCT-1996; 96WO-US015921.

PR 06-OCT-1995; 95US-00541033.

(UYFL ) UNIV FLORIDA.

Schmidt RR, Miller P;

WPI; 1997-226226/20.

N-PSDB; AAT64548.

DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism plant cells.

Claim 1; Page 48-50; 61pp; English.

2 Polypeptides (AAW15411 and AAW15412) respectively comprise the mature alpha subunit (AAW15407) and beta subunit (AAW15408) proteins of an ammonium-inducible, chloroplast-localised hexameric NADP-specific glutamate dehydrogenase (NADP-GDH) isoenzymes of Chlorella sorokiniana. They are produced by removal of transit peptides from the precursor proteins (AAW15407-08). The N metabolism of plants can be modulated (pref. increasing the assimilation of inorganic N into organic N) by transforming them with nucleotide sequences (see also AAT64529-30, AAT64547-48) encoding the alpha and/or beta subunits or precursor proteins. Such plants show improved properties, e.g. increased crop yield and improved stress tolerance. Heterohexamers having alpha and beta



CC subunits can be expressed that have higher aminating/deaminating activity  
 CC ratios (i.e. higher capacity for glutamate synthesis) than homohexamers.  
 CC (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 476 AA;

Query Match 100.0%; Score 2465; DB 2; Length 476;  
 Best Local Similarity 100.0%; Pred. No. 3e-228;  
 Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDATTGDFALQKAVKQMATKAGTEGLVHGINKNPVDRQLLTETIFMKDPEQEFMQAVREV 60  
 DB 1 MDATTGDFALQKAVKQMATKAGTEGLVHGINKNPVDRQLLTETIFMKDPEQEFMQAVREV 60

QY 61 AVSLQPVFEKRPPELLPIFKQIVPEPRTVFRVSWLDDAGNLQVNRGRFRVQYSSAIGPYKG 120  
 DB 61 AVSLQPVFEKRPPELLPIFKQIVPEPRTVFRVSWLDDAGNLQVNRGRFRVQYSSAIGPYKG 120

QY 121 GLRPHPSVNLSTMKFLAFEQIFKNSLTTLPMGGKGSGDFDPKGSDAEVMRFQCSFMT 180  
 DB 121 GLRPHPSVNLSTMKFLAFEQIFKNSLTTLPMGGKGSGDFDPKGSDAEVMRFQCSFMT 180

QY 181 LQRHISYVQDVPAGDIGVGAREIGVLFQYKRTKNYTGVLTPKGQEGSGSEIRPEATGY 240  
 DB 181 LQRHISYVQDVPAGDIGVGAREIGVLFQYKRTKNYTGVLTPKGQEGSGSEIRPEATGY 240

QY 241 GAVLFVENVLKDGESLKGKCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG 300  
 DB 241 GAVLFVENVLKDGESLKGKCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG 300

QY 301 FTREQLQAVQDMKKNNNSARISEYKSDTAVVVGDRRKPWELDCQVDIAPPCCATQNEIDEH 360  
 DB 301 FTREQLQAVQDMKKNNNSARISEYKSDTAVVVGDRRKPWELDCQVDIAPPCCATQNEIDEH 360

QY 361 DAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIICPGKAANAGGVAVSGLEMTQNRMS 420  
 DB 361 DAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIICPGKAANAGGVAVSGLEMTQNRMS 420

QY 421 LNWTRREEVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTTKVADAVKAQGAV 476  
 DB 421 LNWTRREEVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTTKVADAVKAQGAV 476

# RESULT 2

AAU98955  
 ID AAU98955 standard; protein; 476 AA.

XX AAU98955;

AC AAU98955;

DT 24-SEP-2002 (first entry)

DE Mature NADP-glutamate dehydrogenase beta subunit.

XX NADP-specific glutamate dehydrogenase; NADP-GDH; beta subunit; alga;

KW nitrogen metabolism; plant; ammonium assimilation; transgenic;

KW ammonia toxicity tolerance; osmotic stress tolerance; enzyme.

XX Chlorella sorokiniana.

XX US2002062495-A1.

XX 23-MAY-2002.

XX 01-MAY-1998; 98US-00070844.

XX 01-MAY-1998; 98US-00070844.

XX (SCHW/) SCHWIDT R R.

XX (MILL/) MILLER P.

XX Schmidt RR, Miller P;

XX WPI; 2002-499691/53.

DR N-PSDB; ABK51026.

XX Transforming a plant with a polynucleotide encoding a polypeptide with  
 PT glutamate dehydrogenase activity provides a plant with modulated nitrogen  
 PT metabolism useful to increase yield and ammonium and osmotic stress  
 PT tolerance.

XX Claim 7; Page 31-32; 35pp; English.

XX The invention relates to a method of modulating nitrogen metabolism in  
 CC plant cells, comprising transforming a plant cell with a polynucleotide  
 CC encoding a polypeptide having glutamate dehydrogenase activity, and  
 CC culturing the cell to produce descendant cells which express the  
 CC polypeptide. The method is used to provide plants with increased yield,  
 CC improved ammonium assimilation properties, increased tolerance to ammonia  
 CC toxicity, improved osmotic stress tolerance and improved composition. The  
 CC present sequence represents the amino acid sequence of Chlorella  
 CC sorokiniana mature NADP-glutamate dehydrogenase beta subunit, used in the  
 CC method of the invention

XX Sequence 476 AA;

Query Match 100.0%; Score 2465; DB 5; Length 476;  
 Best Local Similarity 100.0%; Pred. No. 3e-228;  
 Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDATTGDFALQKAVKQMATKAGTEGLVHGINKNPVDRQLLTETIFMKDPEQEFMQAVREV 60

DB 1 MDATTGDFALQKAVKQMATKAGTEGLVHGINKNPVDRQLLTETIFMKDPEQEFMQAVREV 60

QY 61 AVSLQPVFEKRPPELLPIFKQIVPEPRTVFRVSWLDDAGNLQVNRGRFRVQYSSAIGPYKG 120

DB 61 AVSLQPVFEKRPPELLPIFKQIVPEPRTVFRVSWLDDAGNLQVNRGRFRVQYSSAIGPYKG 120

QY 121 GLRPHPSVNLSTMKFLAFEQIFKNSLTTLPMGGKGSGDFDPKGSDAEVMRFQCSFMT 180

DB 121 GLRPHPSVNLSTMKFLAFEQIFKNSLTTLPMGGKGSGDFDPKGSDAEVMRFQCSFMT 180

QY 181 LQRHISYVQDVPAGDIGVGAREIGVLFQYKRTKNYTGVLTPKGQEGSGSEIRPEATGY 240

DB 181 LQRHISYVQDVPAGDIGVGAREIGVLFQYKRTKNYTGVLTPKGQEGSGSEIRPEATGY 240

QY 241 GAVLFVENVLKDGESLKGKCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG 300

DB 241 GAVLFVENVLKDGESLKGKCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG 300

QY 301 FTREQLQAVQDMKKNNNSARISEYKSDTAVVVGDRRKPWELDCQVDIAPPCCATQNEIDEH 360

DB 301 FTREQLQAVQDMKKNNNSARISEYKSDTAVVVGDRRKPWELDCQVDIAPPCCATQNEIDEH 360

QY 361 DAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIICPGKAANAGGVAVSGLEMTQNRMS 420

DB 361 DAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIICPGKAANAGGVAVSGLEMTQNRMS 420

QY 421 LNWTRREEVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTTKVADAVKAQGAV 476

DB 421 LNWTRREEVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTTKVADAVKAQGAV 476

# RESULT 3

ADQ36731  
 ID ADQ36731 standard; protein; 476 AA.

XX ADQ36731;

XX 23-SEP-2004 (first entry)

XX Mature NADP-specific GDH beta subunit, SEQ ID 26.

XX Nitrogen metabolism; plant; glutamate dehydrogenase; GDH; enzyme;

KW beta subunit; NADP-specific GDH; NADP-specific glutamate dehydrogenase.

XX Chlorella sorokiniana.

```
XX  US2004128710-A1.
XX  01-JUL-2004.
XX  24-JUL-2003; 2003US-00627886.
XX  01-MAY-1998; 98US-00070844.
XX  (SCHM/) SCHMIDT R R.
XX  (MILL/) MILLER P.
XX  Schmidt RR, Miller P;
XX  WPI; 2004-533134/51.
XX  N-PSDB; ADQ36730.
XX  Increasing or decreasing nitrogen metabolism in plant cells, for plant
XX  with increased yield and improved tolerance to ammonia toxicity and
XX  osmotic stress, by transforming plant cell with nucleic acid having
XX  glutamate dehydrogenase activity.
XX  Claim 7; SEQ ID NO 26; 36pp; English.
XX  The present invention relates to increasing or decreasing the nitrogen
XX  metabolism in plant cells by transforming a plant cell with a
XX  polynucleotide encoding a polypeptide having glutamate dehydrogenase
XX  (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH
XX  (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709,
XX  ADQ36731), or their fragments, which exhibits GDH activity. The
XX  polynucleotide is operably linked to a polynucleotide encoding a
XX  chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their
XX  fragments that exhibit chloroplast transit activity. The method is useful
XX  for increasing or decreasing the nitrogen metabolism in plant cells. The
XX  methods, polynucleotides, and polypeptides are useful in producing plant
XX  with increased yield, and with improved tolerance to ammonia toxicity,
XX  osmotic stress, and composition of the crop or plant. The present
XX  sequence is the mature beta subunit of the NADP-specific GDH used in the
XX  method of the invention.
XX  Sequence 476 AA;
XX  Query Match 100.0%; Score 2465; DB 8; Length 476;
XX  Best Local Similarity 100.0%; Pred. No. 3e-228;
XX  Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKPNPDVRLTTEIFMKDPQQFMOQAVREV 60
DB 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKPNPDVRLTTEIFMKDPQQFMOQAVREV 60
QY 61 AVSLQPVFEKRPPELLPIFKQIVPEPVTITFRVSWLDDAGNLQVNRGFRVOYSSAIGPYKG 120
DB 61 AVSLQPVFEKRPPELLPIFKQIVPEPVTITFRVSWLDDAGNLQVNRGFRVOYSSAIGPYKG 120
QY 121 GLRFHPSVNLISIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVWRFQCSFMTE 180
DB 121 GLRFHPSVNLISIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVWRFQCSFMTE 180
QY 181 LQRHISYQDVDPAGDITGVGAREIGYLFQGYKRTKNYTGVLTPKGQYCGSEIRPEATGY 240
DB 181 LQRHISYQDVDPAGDITGVGAREIGYLFQGYKRTKNYTGVLTPKGQYCGSEIRPEATGY 240
QY 241 GAVLFVENVLKDGESLKGKRLVSGAGNVAQYCAELLEKGAIVLISLSDSQSYVYEPNG 300
DB 241 GAVLFVENVLKDGESLKGKRLVSGAGNVAQYCAELLEKGAIVLISLSDSQSYVYEPNG 300
QY 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRLKPMELDCQVDIAPPCATQNEIDSH 360
DB 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRLKPMELDCQVDIAPPCATQNEIDSH 360
QY 361 DABLLIKHGQYVVEGANNPSTNEAITHKYNKAGIITCPGKAANAGGAVVSGLEMTQNRMS 420
DB 361 DABLLIKHGQYVVEGANNPSTNEAITHKYNKAGIITCPGKAANAGGAVVSGLEMTQNRMS 420
QY 421 LNWTRREVRDKLERIMKDIYDSAMGPSRRYNNVDLAAGANIAGFTTKVADAVKAQGAV 476
DB 421 LNWTRREVRDKLERIMKDIYDSAMGPSRRYNNVDLAAGANIAGFTTKVADAVKAQGAV 476
XX  RESULT 4
XX  AAU98954
XX  ID AAU98954 standard; protein; 487 AA.
XX  AC AAU98954;
XX  DT 24-SEP-2002 (first entry)
XX  DE Mature NADP-glutamate dehydrogenase alpha subunit.
XX  KW NADP-specific glutamate dehydrogenase; NADP-GDH; alpha subunit; alga;
XX  nitrogen metabolism; plant; ammonium assimilation; transgenic;
XX  ammonia toxicity tolerance; osmotic stress tolerance; enzyme.
XX  OS Chlorella sorokiniana.
XX  PN US20020262495-A1.
XX  PD 23-MAY-2002.
XX  PF 01-MAY-1998; 98US-00070844.
XX  PR 01-MAY-1998; 98US-00070844.
XX  (SCHM/) SCHMIDT R R.
XX  (MILL/) MILLER P.
XX  Schmidt RR, Miller P;
XX  WPI; 2002-499691/53.
XX  N-PSDB; ABK51025.
XX  Transforming a plant with a polynucleotide encoding a polypeptide with
XX  glutamate dehydrogenase activity provides a plant with modulated nitrogen
XX  metabolism useful to increase yield and ammonium and osmotic stress
XX  tolerance.
XX  Claim 7; Page 27-28; 35pp; English.
XX  The invention relates to a method of modulating nitrogen metabolism in
XX  plant cells, comprising transforming a plant cell with a polynucleotide
XX  encoding a polypeptide having glutamate dehydrogenase activity, and
XX  culturing the cell to produce descendant cells which express the
XX  polypeptide. The method is used to provide plants with increased yield,
XX  improved ammonium assimilation properties, increased tolerance to ammonia
XX  toxicity, improved osmotic stress tolerance and improved composition. The
XX  present sequence represents the amino acid sequence of Chlorella
XX  sorokiniana mature NADP-glutamate dehydrogenase alpha subunit, used in
XX  the method of the invention
XX  Sequence 487 AA;
XX  Query Match 100.0%; Score 2465; DB 5; Length 487;
XX  Best Local Similarity 100.0%; Pred. No. 3.1e-228;
XX  Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKPNPDVRLTTEIFMKDPQQFMOQAVREV 60
DB 12 MDATTGDTALQKAVKQMATKAGTEGLVHGINKPNPDVRLTTEIFMKDPQQFMOQAVREV 71
QY 61 AVSLQPVFEKRPPELLPIFKQIVPEPVTITFRVSWLDDAGNLQVNRGFRVOYSSAIGPYKG 120
DB 72 AVSLQPVFEKRPPELLPIFKQIVPEPVTITFRVSWLDDAGNLQVNRGFRVOYSSAIGPYKG 131
QY 121 GLRFHPSVNLISIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVWRFQCSFMTE 180
DB 132 GLRFHPSVNLISIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVWRFQCSFMTE 191
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QY 181 LQRHISYVQDVDPAGDIGVAREIGYLFQYKRTKNTYTGVLTPKQGEYCGSIRPEATGY 240  
 DB 192 LQRHISYVQDVDPAGDIGVAREIGYLFQYKRTKNTYTGVLTPKQGEYCGSIRPEATGY 251  
 QY 241 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQYVYEPNG 300  
 DB 252 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQYVYEPNG 311  
 QY 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCCATQNEIDEH 360  
 DB 312 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCCATQNEIDEH 371  
 QY 361 DAELLIKHGCOYVVEGANMPSNEAIHKYNKAGIYCPCGAANAGGAVVSGLEMTQNRMS 420  
 DB 372 DAELLIKHGCOYVVEGANMPSNEAIHKYNKAGIYCPCGAANAGGAVVSGLEMTQNRMS 431  
 QY 421 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTTKVADAVKAQGAV 476  
 DB 432 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTTKVADAVKAQGAV 487

## RESULT 5

ADQ36729  
 ID ADQ36729 standard; protein; 487 AA.  
 XX AC ADQ36729;  
 XX DT 23-SEP-2004 (first entry)  
 XX DE Mature NADP-specific GDH alpha subunit, SEQ ID 24.  
 XX KW Nitrogen metabolism; plant; glutamate dehydrogenase; GDH; enzyme;  
 XX KW alpha subunit; NADP-specific GDH; NADP-specific glutamate dehydrogenase.  
 XX OS Chlorella sorokiniana.  
 XX PN US2004128710-A1.  
 XX PD 01-JUL-2004.  
 XX PF 24-JUL-2003; 2003US-00627886.  
 XX PR 01-MAY-1998; 98US-00070844.  
 XX PA (SCHM/) SCHMIDT R R.  
 XX PA (MILL/) MILLER P.  
 XX PI Schmidt RR, Miller P;  
 XX DR WPI, 2004-533134/51.  
 XX DR N-PSDB; ADQ36728.

XX Increasing or decreasing nitrogen metabolism in plant cells, for plant  
 PT with increased yield and improved tolerance to ammonia toxicity and  
 PT osmotic stress, by transforming plant cell with nucleic acid having  
 PT Glutamate dehydrogenase activity.  
 XX Claim 7; SEQ ID NO 24; 36pp; English.  
 XX The present invention relates to increasing or decreasing the nitrogen  
 CC metabolism in plant cells by transforming a plant cell with a  
 CC polynucleotide encoding a polypeptide having glutamate dehydrogenase  
 CC (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH  
 CC (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709,  
 CC ADQ36731), or their fragments, which exhibits GDH activity. The  
 CC polynucleotide is operably linked to a polynucleotide encoding a  
 CC chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their  
 CC fragments that exhibit chloroplast transit activity. The method is useful  
 CC for increasing or decreasing the nitrogen metabolism in plant cells. The  
 CC methods, polynucleotides, and polypeptides are useful in producing plant  
 CC with increased yield, and with improved tolerance to ammonia toxicity,  
 CC osmotic stress, and composition of the crop or plant. The present

CC sequence is the mature alpha subunit of the NADP-specific GDH used in the  
 CC method of the invention.

XX SQ Sequence 487 AA;

Query Match 100.0%; Score 2465; DB 8; Length 487;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-228;  
 Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDATGDTALQKAVKQMATKAGTEGLVHGINKNPDPVROLTEIFMKDPEQBEFMAQVREV 60  
 DB 12 MDATGDTALQKAVKQMATKAGTEGLVHGINKNPDPVROLTEIFMKDPEQBEFMAQVREV 71  
 QY 61 AVSLQPVPEKPELLPIFKQIVPEPERVITFRVSWLDDAGNLQVNRGPRVQYSSAIGPYKG 120  
 DB 72 AVSLQPVPEKPELLPIFKQIVPEPERVITFRVSWLDDAGNLQVNRGPRVQYSSAIGPYKG 131  
 QY 121 GLRFHPSVNLSTIMKFLAFEQIFKNSLTTLPMGGGKGGSDPDPKGSDAEVMRFCSFWTE 180  
 DB 132 GLRFHPSVNLSTIMKFLAFEQIFKNSLTTLPMGGGKGGSDPDPKGSDAEVMRFCSFWTE 191  
 QY 181 LQRHISYVQDVDPAGDIGVAREIGYLFQYKRTKNTYTGVLTPKQGEYCGSIRPEATGY 240  
 DB 192 LQRHISYVQDVDPAGDIGVAREIGYLFQYKRTKNTYTGVLTPKQGEYCGSIRPEATGY 251  
 QY 241 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQYVYEPNG 300  
 DB 252 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQYVYEPNG 311  
 QY 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCCATQNEIDEH 360  
 DB 312 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCCATQNEIDEH 371  
 QY 361 DAELLIKHGCOYVVEGANMPSNEAIHKYNKAGIYCPCGAANAGGAVVSGLEMTQNRMS 420  
 DB 372 DAELLIKHGCOYVVEGANMPSNEAIHKYNKAGIYCPCGAANAGGAVVSGLEMTQNRMS 431  
 QY 421 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTTKVADAVKAQGAV 476  
 DB 432 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTTKVADAVKAQGAV 487

## RESULT 6

AAW15408  
 ID AAW15408 standard; protein; 512 AA.  
 XX AC AAW15408;  
 XX DT 17-OCT-2003 (revised)  
 XX DT 10-JUL-1997 (first entry)  
 XX DE NADP-specific glutamate dehydrogenase beta-subunit precursor.  
 XX KW Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;  
 XX KW chloroplast; transgenic plant.  
 XX OS Chlorella sorokiniana; strain UTEX 1230.

XX WO9712983-A1.

XX PD 10-APR-1997.

XX PF 03-OCT-1996; 96WO-US015921.

XX PR 06-OCT-1995; 95US-00541033.

XX PA (UYFL ) UNIV FLORIDA.

XX PI Schmidt RR, Miller P;

XX DR WPI; 1997-226226/20.

XX DR N-PSDB; AAT64530, AAT64543.

PT DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella  
PT sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism  
PT plant cells.  
PS Claim 1; Page 29-32; 61pp; English.  
XX  
XX  
XX 2 Polypeptides (AAW15407 and AAW15408) respectively comprise the alpha  
CC (AAW15407) and beta subunit (AAW15408) precursor proteins of an ammonium-  
CC inducible, chloroplast-localised NADP-specific glutamate dehydrogenase  
CC (NADP-GDH) of Chlorella sorokiniana. They are processed to mature alpha  
CC and beta subunits (see also AAW15411-12) that comprise the active NADP-  
CC GDH hexameric isoenzymes. The N metabolism of plants can be modulated  
CC (pref. increasing the assimilation of inorganic N into organic N) by  
CC transforming them with nucleotide sequences (see also AAW15429-30,  
CC AAW15447-48) encoding the alpha and/or beta subunits or precursor  
CC proteins. Such plants show improved properties, e.g. increased crop yield  
CC and improved stress tolerance. Heterohexamers having alpha and beta  
CC subunits can be expressed that have higher aminating/deaminating activity  
CC ratios (i.e. higher capacity for glutamate synthesis) than homohexamers.  
CC (updated on 17-OCT-2003 to standardise OS field)  
XX Sequence 512 AA;

Query Match 100.0%; Score 2465; DB 2; Length 512;  
Best Local Similarity 100.0%; Pred. No. 3.4e-228;  
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKNPDVRLQLTEIFMKDPQQBFMQAVREV 60  
Db 37 MDATTGDTALQKAVKQMATKAGTEGLVHGINKNPDVRLQLTEIFMKDPQQBFMQAVREV 96  
QY 61 AVSLQPVFEKRPPELLPIFKQIVPEPVRTVFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120  
Db 97 AVSLQPVFEKRPPELLPIFKQIVPEPVRTVFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 156  
QY 121 GLRFHPSVNLSTIMKFLAFEQIFKNSLTTLPMGGGKGGSDFPKGSDAEVMRFCSFMT 180  
Db 157 GLRFHPSVNLSTIMKFLAFEQIFKNSLTTLPMGGGKGGSDFPKGSDAEVMRFCSFMT 216  
QY 181 LQRHSYVQDVPAGDIGVGAREIGYLFQYKRITKNYTVGLTPKQEGSGSIRPEATGY 240  
Db 217 LQRHSYVQDVPAGDIGVGAREIGYLFQYKRITKNYTVGLTPKQEGSGSIRPEATGY 276  
QY 241 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLEKGAI VLSLSDSQGYVPEP 300  
Db 277 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLEKGAI VLSLSDSQGYVPEP 336  
QY 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRLKRWELDCQVDIAPPCATQNEIDEH 360  
Db 337 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRLKRWELDCQVDIAPPCATQNEIDEH 396  
QY 361 DAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIIPCCKAANAGGAVVSGLEMTQNRMS 420  
Db 397 DAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIIPCCKAANAGGAVVSGLEMTQNRMS 456  
QY 421 LNWTRVEVRDKLERIMKDIYDSAMGSPRRYNYDLAAGANIAGFTKVADAVKAQGA 476  
Db 457 LNWTRVEVRDKLERIMKDIYDSAMGSPRRYNYDLAAGANIAGFTKVADAVKAQGA 512

RESULT 7  
AAU98951  
ID AAU98951 standard; protein; 512 AA.  
XX  
AC AAU98951;  
XX  
XX 24-SEP-2002 (first entry)  
XX NADP-glutamate dehydrogenase beta subunit.  
XX NADP-specific glutamate dehydrogenase; NADP-GDH; beta subunit; alga;  
KW nitrogen metabolism; plant; ammonium assimilation; transgenic;  
KW ammonia toxicity tolerance; osmotic stress tolerance; enzyme.

XX Chlorella sorokiniana.  
XX US2002062495-A1.  
XX 23-MAY-2002.  
XX  
XX 01-MAY-1998; 98US-00070844.  
XX 01-MAY-1998; 98US-00070844.  
XX (SCHM/) SCHMIDT R R.  
XX (MILL/) MILLER P.  
XX Schmidt RR, Miller P;  
XX WPI; 2002-499691/53.  
XX N-PSDB; ABK51008.  
XX  
XX Transforming a plant with a polynucleotide encoding a polypeptide with  
PT glutamate dehydrogenase activity provides a plant with modulated nitrogen  
PT metabolism useful to increase yield and ammonium and osmotic stress  
PT tolerance.  
XX Claim 6; Page 17-18; 35pp; English.  
XX  
XX The invention relates to a method of modulating nitrogen metabolism in  
CC plant cells, comprising transforming a plant cell with a polynucleotide  
CC encoding a polypeptide having glutamate dehydrogenase activity, and  
CC culturing the cell to produce descendant cells which express the  
CC polypeptide. The method is used to provide plants with increased yield,  
CC improved ammonium assimilation properties, increased tolerance to ammonia  
CC toxicity, improved osmotic stress tolerance and improved composition. The  
CC present sequence represents the amino acid sequence of Chlorella  
CC sorokiniana NADP-glutamate dehydrogenase beta subunit, used in the method  
CC of the invention  
XX Sequence 512 AA;

Query Match 100.0%; Score 2465; DB 5; Length 512;  
Best Local Similarity 100.0%; Pred. No. 3.4e-228;  
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKNPDVRLQLTEIFMKDPQQBFMQAVREV 60  
Db 37 MDATTGDTALQKAVKQMATKAGTEGLVHGINKNPDVRLQLTEIFMKDPQQBFMQAVREV 96  
QY 61 AVSLQPVFEKRPPELLPIFKQIVPEPVRTVFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120  
Db 97 AVSLQPVFEKRPPELLPIFKQIVPEPVRTVFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 156  
QY 121 GLRFHPSVNLSTIMKFLAFEQIFKNSLTTLPMGGGKGGSDFPKGSDAEVMRFCSFMT 180  
Db 157 GLRFHPSVNLSTIMKFLAFEQIFKNSLTTLPMGGGKGGSDFPKGSDAEVMRFCSFMT 216  
QY 181 LQRHSYVQDVPAGDIGVGAREIGYLFQYKRITKNYTVGLTPKQEGSGSIRPEATGY 240  
Db 217 LQRHSYVQDVPAGDIGVGAREIGYLFQYKRITKNYTVGLTPKQEGSGSIRPEATGY 276  
QY 241 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLEKGAI VLSLSDSQGYVPEP 300  
Db 277 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLEKGAI VLSLSDSQGYVPEP 336  
QY 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRLKRWELDCQVDIAPPCATQNEIDEH 360  
Db 337 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRLKRWELDCQVDIAPPCATQNEIDEH 396  
QY 361 DAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIIPCCKAANAGGAVVSGLEMTQNRMS 420  
Db 397 DAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIIPCCKAANAGGAVVSGLEMTQNRMS 456  
QY 421 LNWTRVEVRDKLERIMKDIYDSAMGSPRRYNYDLAAGANIAGFTKVADAVKAQGA 476  
Db 457 LNWTRVEVRDKLERIMKDIYDSAMGSPRRYNYDLAAGANIAGFTKVADAVKAQGA 512

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Db      457 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGAV 512

RESULT 8
ADQ36709
ID      ADQ36709 standard; protein; 512 AA.
XX
AC      ADQ36709;
XX
DT      23-SEP-2004 (first entry)
XX
DE      NADP-specific GDH beta subunit precursor protein, SEQ ID 4.
XX
KW      Nitrogen metabolism; plant; glutamate dehydrogenase; GDH; enzyme;
XX      beta subunit; NADP-specific GDH; NADP-specific glutamate dehydrogenase.
XX
OS      Chlorella sorokiniana.
XX
PN      US2004128710-A1.
XX
PD      01-JUL-2004.
XX
PF      24-JUL-2003; 2003US-00627886.
XX
PR      01-MAY-1998; 98US-00070844.
XX
PA      (SCHM/) SCHMIDT R R.
XX      (MILL/) MILLER P.
XX
PI      Schmidt RR, Miller P;
XX
WPI, 2004-533134/51.
DR      N-PSDB; ADQ36708.
XX
PT      Increasing or decreasing nitrogen metabolism in plant cells, for plant
PT      with increased yield and improved tolerance to ammonia toxicity and
PT      osmotic stress, by transforming plant cell with nucleic acid having
PT      glutamate dehydrogenase activity.
XX
PS      Claim 7; SEQ ID NO 4; 36pp; English.
XX
CC      The present invention relates to increasing or decreasing the nitrogen
CC      metabolism in plant cells by transforming a plant cell with a
CC      polynucleotide encoding a polypeptide having glutamate dehydrogenase
CC      (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH
CC      (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709,
CC      ADQ36731), or their fragments, which exhibits GDH activity. The
CC      polynucleotide is operably linked to a polynucleotide encoding a
CC      chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their
CC      fragments that exhibit chloroplast transit activity. The method is useful
CC      for increasing or decreasing the nitrogen metabolism in plant cells. The
CC      methods, polynucleotides, and polypeptides are useful in producing plant
CC      with increased yield, and with improved tolerance to ammonia toxicity,
CC      osmotic stress, and composition of the crop or plant. The present
CC      sequence is the precursor protein of the beta subunit of the NADP-
CC      specific GDH, which is then processed to produce the mature alpha subunit
CC      of the NADP-specific GDH, used in the method of the invention.
XX
SQ      Sequence 512 AA;

Query Match      100.0%; Score 2465; DB 8; Length 512;
Best Local Similarity 100.0%; Pred. No. 3.4e-228;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MDATTGDTALQKAVKQMATKAGTGLVHGINKNPVDRQLLTIFMKDPEQEFMQAVREV 60
Db      37 MDATTGDTALQKAVKQMATKAGTGLVHGINKNPVDRQLLTIFMKDPEQEFMQAVREV 96
QY      61 AVSLQPVFKRPPELLPIPKQIIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
Db      97 AVSLQPVFKRPPELLPIPKQIIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 156
QY      121 GLRFHPSVNLISIMKFLAFEQIFKNSLTTLPMGGKGSGSDFDPKGSDAEVMRFQSPWTE 180

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Db      157 GLRFHPSVNLISIMKFLAFEQIFKNSLTTLPMGGKGSGSDFDPKGSDAEVMRFQSPWTE 216
QY      181 LQRHISYVQDVPAGDIGVGAREIGYLFQGYKRITKNYTGVLTPKGQEGYGGSEIRPEATGY 240
Db      217 LQRHISYVQDVPAGDIGVGAREIGYLFQGYKRITKNYTGVLTPKGQEGYGGSEIRPEATGY 276
QY      241 GAVLFVENVLKDKGESLKGKRCCLVSGAGNVAQYCAELLLLEKGAIVLSLSDSQGYVYEPNG 300
Db      277 GAVLFVENVLKDKGESLKGKRCCLVSGAGNVAQYCAELLLLEKGAIVLSLSDSQGYVYEPNG 336
QY      301 FTRSQLQAVQDMKKKNSARISEYKSDTAVVVGRRKPKWELDCQVDIAFPCCATONEIDEH 360
Db      337 FTRSQLQAVQDMKKKNSARISEYKSDTAVVVGRRKPKWELDCQVDIAFPCCATONEIDEH 396
QY      361 DAELLIKHGCCYVVEGANMPSTNEAIHKYNKAGIYICPGAANAGGVAVSGLEMTQNRMS 420
Db      397 DAELLIKHGCCYVVEGANMPSTNEAIHKYNKAGIYICPGAANAGGVAVSGLEMTQNRMS 456
QY      421 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGAV 476
Db      457 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGAV 512

RESULT 9
AAW15407
ID      AAW15407 standard; protein; 526 AA.
XX
AC      AAW15407;
XX
DT      17-OCT-2003 (revised)
DT      10-JUL-1997 (first entry)
XX
DE      NADP-specific glutamate dehydrogenase alpha-subunit precursor.
XX
KW      Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;
KW      chloroplast; transgenic plant.
XX
OS      Chlorella sorokiniana; strain UTEX 1230.
XX
PN      WO9712983-A1.
XX
PD      10-APR-1997.
XX
PF      03-OCT-1996; 96WO-US015921.
XX
PR      06-OCT-1995; 95US-00541033.
XX
PA      (UYFL ) UNIV FLORIDA.
XX
PI      Schmidt RR, Miller P;
XX
WPI, 1997-226226/20.
DR      N-PSDB; AAT64529, AAT64542.
XX
DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella
PT      sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism
PT      plant cells.
XX
PS      Claim 1; Page 25-27; 61pp; English.
XX
CC      2 Polypeptides (AAW15407 and AAW15408) respectively comprise the alpha
CC      (AAW15407) and beta subunit (AAW15408) precursor proteins of an ammonium-
CC      inducible, chloroplast-localised NADP-specific glutamate dehydrogenase
CC      (NADP-GDH) of Chlorella sorokiniana. They are processed to mature alpha
CC      and beta subunits (see also AAW15411-12) that comprise the active NADP-
CC      GDH hexameric isoenzymes. The N metabolism of plants can be modulated
CC      (pref. increasing the assimilation of inorganic N into organic N) by
CC      transforming them with nucleotide sequences (see also AAT64529-30,
CC      AAT64547-48) encoding the alpha and/or beta subunits or precursor
CC      proteins. Such plants show improved properties, e.g. increased crop yield
CC      and improved stress tolerance. Heterohexamers having alpha and beta
CC      subunits can be expressed that have higher aminating/deaminating activity

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|           |   |
|-----------|---|
| CC        | ratios (i.e. higher capacity for glutamate synthesis) than homoexamers. |
| CC        | (Updated on 17-OCT-2003 to standardise OS field)                        |
| XX        | Sequence 526 AA;  |
| SQ        |   |
|           | Query Match 100.0%; Score 2465; DB 2; Length 526;                       |
|           | Best Local Similarity 100.0%; Pred. No. 3.5e-228;                       |
|           | Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |
| QY        | 1 MDATTGDF TALQKAVKQMATKAGTEGLVHGINKNPVRLQLTIFMKDPEQBFMQAVREV 60        |
| DB        | 51 MDATTGDF TALQKAVKQMATKAGTEGLVHGINKNPVRLQLTIFMKDPEQBFMQAVREV 110      |
| QY        | 61 AVSLQPVFEKRPPELLPIFKQIVPEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120   |
| DB        | 111 AVSLQPVFEKRPPELLPIFKQIVPEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 170  |
| QY        | 121 GLRFHPSVNLSTMKFLAFEQIFKNSLTTLPMGGGKGGSDFPDKGSDAEVWRFCSFMTE 180      |
| DB        | 171 GLRFHPSVNLSTMKFLAFEQIFKNSLTTLPMGGGKGGSDFPDKGSDAEVWRFCSFMTE 230      |
| QY        | 181 LQRHSYVQDVPAGDIGVGAREIGYLFQYKRITKNYTGVLTPKGOEYGSSEIRPEATGY 240      |
| DB        | 231 LQRHSYVQDVPAGDIGVGAREIGYLFQYKRITKNYTGVLTPKGOEYGSSEIRPEATGY 290      |
| QY        | 241 GAVLFVENVLKDKGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQYVYEPNG 300    |
| DB        | 291 GAVLFVENVLKDKGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQYVYEPNG 350    |
| QY        | 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAPPCCATQNEIDEH 360    |
| DB        | 351 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAPPCCATQNEIDEH 410    |
| QY        | 361 DAELLIKHGCGYVVEGANPSTNEAIHKYNKAGIICPGKAANAGGAVVSGLEMTQNRMS 420      |
| DB        | 411 DAELLIKHGCGYVVEGANPSTNEAIHKYNKAGIICPGKAANAGGAVVSGLEMTQNRMS 470      |
| QY        | 421 LNWTRREEVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTTKVADAVKAQGA 476       |
| DB        | 471 LNWTRREEVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTTKVADAVKAQGA 526       |
| RESULT 10 |   |
| AAU98950  |   |
| ID        | AAU98950 standard; protein; 526 AA.                                     |
| XX        |   |
| AC        | AAU98950;   |
| XX        |   |
| DT        | 24-SEP-2002 (first entry)   |
| XX        |   |
| DE        | NADP- glutamate dehydrogenase alpha subunit.                            |
| XX        |   |
| KW        | NADP-specific glutamate dehydrogenase; NADP-GDH; alpha subunit; alga;   |
| KW        | nitrogen metabolism; plant; ammonium assimilation; transgenic;          |
| KW        | ammonia toxicity tolerance; osmotic stress tolerance; enzyme.           |
| XX        |   |
| OS        | Chlorella sorokiniana.  |
| XX        |   |
| PN        | US2002062495-A1.  |
| XX        |   |
| PD        | 23-MAY-2002.  |
| XX        |   |
| PF        | 01-MAY-1998; 98US-00070844.   |
| XX        |   |
| PR        | 01-MAY-1998; 98US-00070844.   |
| XX        |   |
| PA        | (SCHM/) SCHMIDT R R.  |
| PA        | (MILL/) MILLER P.   |
| XX        |   |
| PI        | Schmidt RR, Miller P;   |
| XX        |   |
| XX        | WPI; 2002-499691/53.  |
| DR        | N-PSDB; ABK51007.   |

Transforming a plant with a polynucleotide encoding a polypeptide with glutamate dehydrogenase activity provides a plant with modulated nitrogen metabolism useful to increase yield and ammonium and osmotic stress tolerance.

Claim 6; Page 13-15; 35pp; English.

The invention relates to a method of modulating nitrogen metabolism in plant cells, comprising transcribing a plant cell with a polynucleotide encoding a polypeptide having glutamate dehydrogenase activity, and culturing the cell to produce descendant cells which express the polypeptide. The method is used to provide plants with increased yield, improved ammonium assimilation properties, increased tolerance to ammonia toxicity, improved osmotic stress tolerance and improved composition. The present sequence represents the amino acid sequence of Chlorella sorokiniana NADP-glutamate dehydrogenase alpha subunit, used in the method of the invention

Sequence 526 AA;

Query Match 100.0%; Score 2465; DB 5; Length 526;

Best Local Similarity 100.0%; Pred. No. 3.5e-228;

Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDATTGDF TALQKAVKQMATKAGTEGLVHGINKNPVRLQLTIFMKDPEQBFMQAVREV 60

DB 51 MDATTGDF TALQKAVKQMATKAGTEGLVHGINKNPVRLQLTIFMKDPEQBFMQAVREV 110

QY 61 AVSLQPVFEKRPPELLPIFKQIVPEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120

DB 111 AVSLQPVFEKRPPELLPIFKQIVPEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 170

QY 121 GLRFHPSVNLSTMKFLAFEQIFKNSLTTLPMGGGKGGSDFPDKGSDAEVWRFCSFMTE 180

DB 171 GLRFHPSVNLSTMKFLAFEQIFKNSLTTLPMGGGKGGSDFPDKGSDAEVWRFCSFMTE 230

QY 181 LQRHSYVQDVPAGDIGVGAREIGYLFQYKRITKNYTGVLTPKGOEYGSSEIRPEATGY 240

DB 231 LQRHSYVQDVPAGDIGVGAREIGYLFQYKRITKNYTGVLTPKGOEYGSSEIRPEATGY 290

QY 241 GAVLFVENVLKDKGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQYVYEPNG 300

DB 291 GAVLFVENVLKDKGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQYVYEPNG 350

QY 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAPPCCATQNEIDEH 360

DB 351 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAPPCCATQNEIDEH 410

QY 361 DAELLIKHGCGYVVEGANPSTNEAIHKYNKAGIICPGKAANAGGAVVSGLEMTQNRMS 420

DB 411 DAELLIKHGCGYVVEGANPSTNEAIHKYNKAGIICPGKAANAGGAVVSGLEMTQNRMS 470

QY 421 LNWTRREEVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTTKVADAVKAQGA 476

DB 471 LNWTRREEVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTTKVADAVKAQGA 526

RESULT 11

ADQ36707

ID ADQ36707 standard; protein; 526 AA.

XX

AC ADQ36707;

XX

DT 23-SEP-2004 (first entry)

XX

DE NADP-specific GDH alpha subunit precursor protein, SEQ ID 2.

XX

KW Nitrogen metabolism; plant; glutamate dehydrogenase; GDH; enzyme;

KW alpha subunit; NADP-specific GDH; NADP-specific glutamate dehydrogenase.

XX

XX Chlorella sorokiniana.

XX



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PN US2004128710-A1.
XX
PD
XX
XX 01-JUL-2004.
XX
XX 24-JUL-2003; 2003US-00627886.
XX
XX 01-MAY-1998; 98US-00070844.
XX
XX (SCHM/) SCHMIDT R R.
XX (MILL/) MILLER P.
XX
XX Schmidt RR, Miller P;
XX
XX WPI, 2004-533134/51.
XX N-PSDB; ADQ36706.
XX
XX Increasing or decreasing nitrogen metabolism in plant cells, for plant
XX with increased yield and improved tolerance to ammonia toxicity and
XX osmotic stress, by transforming plant cell with nucleic acid having
XX glutamate dehydrogenase activity.
XX
XX Claim 7; SEQ ID NO 2; 36pp; English.
XX
XX The present invention relates to increasing or decreasing the nitrogen
XX metabolism in plant cells by transforming a plant cell with a
XX polynucleotide encoding a polypeptide having glutamate dehydrogenase
XX (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH
XX (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709,
XX ADQ36731), or their fragments, which exhibits GDH activity. The
XX polynucleotide is operably linked to a polynucleotide encoding a
XX chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their
XX fragments that exhibit chloroplast transit activity. The method is useful
XX for increasing or decreasing the nitrogen metabolism in plant cells. The
XX methods, polynucleotides, and polypeptides are useful in producing plant
XX with increased yield, and with improved tolerance to ammonia toxicity,
XX osmotic stress, and composition of the crop or plant. The present
XX sequence is the precursor protein of the alpha subunit of the NADP-
XX specific GDH, which is then processed to produce the mature alpha subunit
XX of the NADP-specific GDH, used in the method of the invention.
XX
XX Sequence 526 AA;
XX
XX Query Match 100.0%; Score 2465; DB 8; Length 526;
XX Best Local Similarity 100.0%; Pred. No. 3.5e-228; Mismatches 0; Indels 0; Gaps 0;
XX Matches 476; Conservative 0;
XX
QY 1 MDATTGDTALQKAVKQMATKAGTGLVHGINKNPDVROLLEIFMKDPEQOEFMQAVREV 60
Db 51 MDATTGDTALQKAVKQMATKAGTGLVHGINKNPDVROLLEIFMKDPEQOEFMQAVREV 110
QY 61 AVSLQPVPEKRPPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
Db 111 AVSLQPVPEKRPPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 170
QY 121 GLRHPSVNLSTIMKFLAPEQIFKNSLTITLPMGGGKGSDPDPKGSDAEVMRFQCSFTE 180
Db 171 GLRHPSVNLSTIMKFLAPEQIFKNSLTITLPMGGGKGSDPDPKGSDAEVMRFQCSFTE 230
QY 181 LQRHISYVQDVDPAGDIGVAREIGYLFQYKRITKNYTGVLTPKQOYGGSEIRPEATGY 240
Db 231 LQRHISYVQDVDPAGDIGVAREIGYLFQYKRITKNYTGVLTPKQOYGGSEIRPEATGY 290
QY 241 GAVLFVENVLKDGSLKGRCLVSGAGNVAQYCAELLEKGAIVLSLSDSQYVYEPNG 300
Db 291 GAVLFVENVLKDGSLKGRCLVSGAGNVAQYCAELLEKGAIVLSLSDSQYVYEPNG 350
QY 301 FTRELQAVQDMKKNNNSARISEYKSDTAVYVGDRLKPNELDCQVDIAPPCATQNEIDEH 360
Db 351 FTRELQAVQDMKKNNNSARISEYKSDTAVYVGDRLKPNELDCQVDIAPPCATQNEIDEH 410
QY 361 DAELLIKHGCOYVVEGANNPSTNEAIHKYNKAGIICPCGAANAGGAVSGLGEMTQNRMS 420
Db 411 DAELLIKHGCOYVVEGANNPSTNEAIHKYNKAGIICPCGAANAGGAVSGLGEMTQNRMS 470

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QY 421 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVDADVKAQGA 476
Db 471 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVDADVKAQGA 526
XX
XX RESULT 12
XX AAW15411
XX ID AAW15411 standard; protein; 487 AA.
XX
XX AC AAW15411;
XX
XX DT 17-OCT-2003 (revised)
XX DT 10-JUL-1997 (first entry)
XX
XX DE NADP-specific glutamate dehydrogenase alpha subunit.
XX
XX KW Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;
XX chloroplast; transgenic plant.
XX
XX OS Chlorella sorokiniana; strain UTEX 1230.
XX
XX PN WO9712983-A1.
XX
XX PD 10-APR-1997.
XX
XX PF 03-OCT-1996; 96WO-US015921.
XX
XX PR 06-OCT-1995; 95US-00541033.
XX
XX PA (UYFL ) UNIV FLORIDA.
XX
XX PI Schmidt RR, Miller P;
XX
XX DR WPI, 1997-226226/20.
XX N-PSDB; AAT64547.
XX
XX PT DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella
XX sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism
XX plant cells.
XX
XX PS Claim 1; Page 44-46; 61pp; English.
XX
XX CC 2 Polypeptides (AAW15411 and AAW15412) respectively comprise the mature
XX alpha subunit (AAW15407) and beta subunit (AAW15408) proteins of an
XX ammonium-inducible, chloroplast-localised hexameric NADP-specific
XX glutamate dehydrogenase (NADP-GDH) isoenzymes of Chlorella sorokiniana.
XX They are produced by removal of transit peptides from the precursor
XX proteins (AAW15407-08). The N metabolism of plants can be modulated
XX (pref. increasing the assimilation of inorganic N into organic N) by
XX transforming them with nucleotide sequences (see also AAT64529-30,
XX AAT64547-48) encoding the alpha and/or beta subunits or precursor
XX proteins. Such plants show improved properties, e.g. increased crop yield
XX and improved stress tolerance. Heterohexamers having alpha and beta
XX subunits can be expressed that have higher aminating/deaminating activity
XX ratios (i.e. higher capacity for glutamate synthesis) than homohexamers.
XX (Updated on 17-OCT-2003 to standardise OS field)
XX
XX SQ Sequence 487 AA;
XX
XX Query Match 99.7%; Score 2457; DB 2; Length 487;
XX Best Local Similarity 99.8%; Pred. No. 1.8e-227;
XX Matches 475; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 MDATTGDTALQKAVKQMATKAGTGLVHGINKNPDVROLLEIFMKDPEQOEFMQAVREV 60
Db 12 MDATTGDTALQKAVKQMATKAGTGLVHGINKNPDVROLLEIFMKDPEQOEFMQAVREV 71
QY 61 AVSLQPVPEKRPPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
Db 72 AVSLQPVPEKRPPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 131
QY 121 GLRHPSVNLSTIMKFLAPEQIFKNSLTITLPMGGGKGSDPDPKGSDAEVMRFQCSFTE 180

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Db 132 GURFHPSVNLINMKFLAFOIPKNSLUTLPMGGKGGSDFPKSGSDAEVMRFCSFMTE 191  
QY 181 LQRHSIYVQDVDPAGDIGVGAREIGYLFQGYKRTTKNYTGVLTTPKQGYGCGSEIRPATCY 240  
Db 192 LQRHSIYVQDVDPAGDIGVGAREIGYLFQGYKRTTKNYTGVLTTPKQGYGCGSEIRPATCY 251  
QY 241 GAVLFVENVLKKGESLKGKRCILVSGAGNVAQYCAELLLKGAIVLSLSDSQGYVPEPNG 300  
Db 252 GAVLFVENVLKKGESLKGKRCILVSGAGNVAQYCAELLLKGAIVLSLSDSQGYVPEPNG 311  
QY 301 FTREQLQAVQDMKKONNSARISYKSDTAVYVGDGRKPWELDCVDIAPPCATQNEIDSH 360  
Db 312 FTREQLQAVQDMKKONNSARISYKSDTAVYVGDGRKPWELDCVDIAPPCATQNEIDSH 371  
QY 361 DAELLKHGCGYVVEGANMPSTNEAIHKYNKAGIYCPGKAANAGGAVVSGLEMTQNRMS 420  
Db 372 DAELLKHGCGYVVEGANMPSTNEAIHKYNKAGIYCPGKAANAGGAVVSGLEMTQNRMS 431  
QY 421 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGA 476  
Db 432 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGA 487

RESULT 13

ABU38763  
ID ABU38763 standard; protein; 445 AA.

AC ABU38763;

XX 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #24290.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

OS Pseudomonas aeruginosa.

XX W0200277183-A2.

XX 03-OCT-2002.

PF 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haseelbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

DR N-PSDB; ACA42633.

XX Claim 25; SEQ ID NO 66687; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 445 AA;

QY Query Match 53.1%; Score 1309; DB 6; Length 445;  
Best Local Similarity 59.2%; Pred. No. 8.2e-117;  
Matches 263; Conservative 55; Mismatches 120; Indels 6; Gaps 4;

QY 36 VRLQTEIFMKDPEQOEPMQAVREVAVSLQVFEKRPBLLP--IFKQIVEPRVITFRVS 93

Db 5 VDAFLERLKRDRDPDQPEFHQAVEEVLRLPFPLEANPHYLEAGITIERIVEPERAILFRVP 64

QY 94 WLDDAGNLQVNRGRVYSSAIGPYKGLGRFHPSVNLISIMKFLAFAQEQLFKNSLTLTPMGG 153

Db 65 WDDQGRVRVARGYRVQMSAIGPYKGLGRFHPSVNLGLKFLAFAQEQLFKNSLTLTPMGG 124

QY 154 KGKGSDFDPKGSDAEVMRFQCSFMTELQRHISYVQDVDPAGDIGVGAREIGYLFQYKRI 213

Db 125 KGKGSDFDPKGSDAEVMRFQCSFMSELRYRHVGADLDVPAGDIGVGAREIGYLFQYKRL 184

QY 214 TKNYTGVLTPKQGYGSGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCILVSGAGNVAQY 273

Db 185 SNQFTSVLTGKLSYGLSIRPEATGFCVYFAQEMLKDRGRGFDGQQRVAISGSGNVAQY 244

QY 274 CAELLLKGAIVLSLSDSQGYVPEPNGFTREQLQAVQDMKKONNSARISEYKSDTAVYVG 333

Db 245 AARKVMEMGGKVISLSDEGTLYABAGLSDQWYLMELKNVRR-GRIREMAEQFSLOPL 303

QY 334 DRRKEWELDCQVDIAPPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAG 393

Db 304 EGRRPWGLAC--DIALPCATQNELDAEDARLLANGCVCAEGANMPSTLEAVDLFLEAG 361

QY 394 IYICPGKAANAGGAVVSGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSA-MGPSRRYVNV 452

Db 362 ILYAPKASNAGGAVVSGLEMSQNAMLRWSEGEVDTKLHGIMQSIHACLLIYGEQGRV 421

QY 453 DLAAGANTAGTKVADAVKAQGA 476

Db 422 NYVKGANTAGTVKADAMLAQGV 445

RESULT 14

ABO71900

ID ABO71900 standard; protein; 450 AA.

XX ABO71900;

XX 29-JUL-2004 (first entry)

DE Pseudomonas aeruginosa polypeptide #4075.

XX Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.

XX OS *Pseudomonas aeruginosa*.  
XX PN US6551795-B1.  
XX PD 22-APR-2003.  
XX PF 18-FEB-1999; 99US-00252991.  
XX PR 18-FEB-1998; 98US-0074788P.  
XX PT 27-JUL-1998; 98US-0094190P.  
XX PA (GENO-) GENOME THERAPEUTICS CORP.  
XX PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;  
XX DR WPI; 2003-615309/58.  
XX DR N-PSDB; ABD05471.  
XX PT Novel isolated nucleic acid encoding *Pseudomonas aeruginosa* polypeptide, of  
XX PT useful as molecular targets for diagnostics, prophylaxis and treatment of  
XX PT pathological conditions resulting from bacterial infection.  
XX PS Disclosure; SEQ ID NO 20646; 455pp; English.  
XX CC The invention relates to *Pseudomonas aeruginosa* polypeptides and the  
XX CC polynucleotides encoding them. The sequences are useful in diagnosis and  
XX CC therapy of pathological conditions, as molecular targets for diagnostics,  
XX CC prophylaxis and treatment of pathological conditions resulting from a  
XX CC bacterial infection, for evaluating a compound, such as a polypeptide,  
XX CC for the ability to bind a *P. aeruginosa* nucleic acid, as components of  
XX CC effective antibacterial targets, as targets for antibacterial drugs,  
XX CC including anti-*P. aeruginosa* drugs, as templates for recombinant  
XX CC production of *P. aeruginosa*-derived peptides or polypeptides, as target  
XX CC components for diagnosis and/or treatment of *P. aeruginosa*-caused  
XX CC infection, and in detection of *P. aeruginosa* sequences or other sequences  
XX CC of *Pseudomonas* species using biochip technology. Sequences ABO67826:  
XX CC ABO84396 represent *P. aeruginosa* polypeptides of the invention. Note: The  
XX CC sequence data for this patent did not form part of the printed  
XX CC specification but was obtained in electronic format from USPTO at  
XX CC seqdata.uspto.gov/sequence.html  
XX SQ Sequence 450 AA;

Query Match 53.1%; Score 1309; DB 7; Length 450;  
Best Local Similarity 59.2%; Pred. No. 8.3e-117;  
Matches 263; Conservative 55; Mismatches 120; Indels 6; Gaps 4;  
QY 36 VRLQLTEIFMKDPEQEEFMAQVREAVSLQVPFEKPELLP--IFKQIVPERVITFRVS 93  
DB 10 VDAFLERLKRDPDQDPFHQAEEVLRSLWPLFANPHYLEAGIIEIVPEPRAILFRVP 69  
QY 94 WLDDAGNLQVNRGFRVQYSSAIGPYKGGIRPHSPVNLSTMKFLAEPQFKNSLTLLPMGG 153  
DB 70 WDDQGRVNRGFRVQYSSAIGPYKGGIRPHSPVNLSTMKFLAEPQFKNSLTLLPMGG 129  
QY 154 KGKGSDFDPKGSADAFVNRFCQSPMTELQRHISYVQDVPAGDIGVAREIGYLFQYKRI 213  
DB 130 KGKGSDFDPKGSADAFVNRFCQSPMTELQRHISYVQDVPAGDIGVAREIGYLFQYKRI 189  
QY 214 TKNYTGVLTPKQEGGSEIRPEATGYGAVLVFVNVLDKGSLSKGLVSGAGNVAQY 273  
DB 190 SNQFTSVLTGKLSYGGSLIRPEATGYGAVLVFVNVLDKGSLSKGLVSGAGNVAQY 249  
QY 274 CAELLEKGAIVLSLSDSGYVYFENGFTREQLQAVQDMKKNNGARISEYKSDTAVVVG 333  
DB 250 AARKVMWGGKVISLSDSEGLYAEAGLSDEQWEIYLMELKNYR--GRTEMAEQSLQFL 308  
QY 334 DRKPKWELDCQVDIAPPATONIEIDHDAELLIKHGCGYVVEGANNPSTNEAIHKYNKAG 393  
DB 309 EGRRWGLAC--DIALPCATONELDAEDARRLLANGCVVAGANNPSTLEAVDLPLEAG 366  
QY 394 IYCFPGKAANAGVAVSGLGEMTQNRMSLNWTREVRDRLKLRIMKDIYDSA-MGPSRRYV 452

DB 367 ILIYAPGRASNAGGVAVSGLGEMTQNRMSLNWTREVRDRLKLRIMKDIYDSA-MGPSRRYV 426  
QY 453 DLAAAGANIAGFTKVADAVKAQGV 476  
DB 427 NYVKGANIAGFPVKVADAMLAQGVV 450  
RESULT 15  
ADP08330  
ID ADP08330 standard; protein; 444 AA.  
XX AC ADP08330;  
XX DT 26-AUG-2004 (first entry)  
XX DE Neisseria meningitidis MCS8 OMV-related membrane protein - SEQ ID 163.  
XX KW outer-membrane vesicle; antibacterial; antiinflammatory;  
XX KW meningococcal protein trafficking; localisation; infection; vaccine;  
XX KW gene therapy.  
XX OS Neisseria meningitidis MCS8.  
XX PN WO2004046177-A2.  
XX PD 03-JUN-2004.  
XX PF 17-NOV-2003; 2003WO-IB006281.  
XX PR 15-NOV-2002; 2002GB-00026734.  
XX PR 27-MAR-2003; 2003GB-00007131.  
XX PA (CHIR ) CHIRON SRL.  
XX PI Norais N, Grandi G;  
XX WPI; 2004-420615/39.  
XX PT New compositions having outer-membrane vesicles and proteins from  
XX PT Neisseria meningitidis, useful in the field of meningococcal  
XX PT biochemistry, in particular for preventing and/or treating meningococcal  
XX PT infections.  
XX PS Claim 9; SEQ ID NO 163; 79pp; English.  
XX CC The invention relates to a novel composition comprising outer-membrane  
XX CC vesicles (OMV) prepared from a first strain of *Neisseria meningitidis* and  
XX CC 1 or more proteins which are present in OMVs prepared from a second  
XX CC strain of *N. meningitidis*, but which are not present in OMVs prepared  
XX CC from the first strain. The composition of the invention demonstrates  
XX CC antibacterial and antiinflammatory activities and may be useful in the  
XX CC field of meningococcal biochemistry, in particular the trafficking and  
XX CC localisation of meningococcal proteins, as well as in the prevention or  
XX CC treatment of meningococcal infections, possibly via the production of a  
XX CC vaccine or gene therapy. The current sequence is that of a *Neisseria*  
XX CC meningitidis MCS8 outer-membrane vesicle (OMV)-related membrane protein  
XX CC of the invention.  
XX SQ Sequence 444 AA;

Query Match 52.8%; Score 1300.5; DB 8; Length 444;  
Best Local Similarity 57.4%; Pred. No. 5.4e-116;  
Matches 257; Conservative 72; Mismatches 104; Indels 15; Gaps 6;  
QY 35 DVROLLTEIFMKDPEQEEFMAQVREAVSLQVPFEKPELLP--PIFKQIVPERVITFRV 92  
DB 3 DLNTLFANLKKORNPQEPFHQAEEVLRSLWPLFANPHYLEAGIIEIVPEPRAILFRVP 62  
QY 93 SWLDDAGNLQVNRGFRVQYSSAIGPYKGGIRPHSPVNLSTMKFLAEPQFKNSLTLLPMG 152  
DB 63 TWQDDKGQVNRGFRVQYSSAIGPYKGGIRPHSPVNLSTMKFLAEPQFKNSLTLLPMG 122

|    |     |              |            |            |            |             |                             |     |
|----|-----|--------------|------------|------------|------------|-------------|-----------------------------|-----|
| Qy | 153 | GGKGSDFDPKGS | DAEYVWRFCQ | SPWTELORHI | SYVDVPAGDI | GVGAREIGYLF | QGYKR                       | 212 |
|    |     | :            | :          | :          | :          | :           | :                           |     |
| Db | 123 | GGKGSDFDPKGS | DAEYVWRFCQ | SPWTELYRHH | GADTVPAGDI | GVGGREIGYLF | QGYKK                       | 182 |
|    |     | :            | :          | :          | :          | :           | :                           |     |
| Qy | 213 | ITKNTYGLTPK  | GQYGGSEIR  | PEATGYCAVL | FVENVLKDG  | ESLKGKRC    | LVSGAGNVAQ                  | 272 |
|    |     | :            | :          | :          | :          | :           | :                           |     |
| Db | 183 | IRNBPSSVLT   | KGLEWGS    | LIRPEATGY  | GCYVFAQ    | AMLQTRND    | SPGKRVLLSGSGNVAQ            | 242 |
|    |     | :            | :          | :          | :          | :           | :                           |     |
| Qy | 273 | YCAELLLEKGA  | IVLSLSD    | SGYVYEP    | -NGFTREOL  | QAOVDM      | KKNKSARISEYKSDTAVY          | 331 |
|    |     | :            | :          | :          | :          | :           | :                           |     |
| Db | 243 | YAAEKAIOLG   | KAVLTV     | SDSNGFVL   | PPDSGWT    | EAQLAALTE   | KEVRRE-RVATYAKEQGLQ         | 301 |
|    |     | :            | :          | :          | :          | :           | :                           |     |
| Qy | 332 | VGDRRKWELD   | QCQVDIA    | PPCATQNB   | EIDHDAEL   | LIKHGQYV    | VEGANPSTNEALHKYNK           | 391 |
|    |     | :            | :          | :          | :          | :           | :                           |     |
| Db | 302 | YFEKQKPGV    | --AAEIAL   | PCATQNB    | DEAAKTL    | LLANGCYV    | VAEGANPSTLGVAEQFIK          | 359 |
|    |     | :            | :          | :          | :          | :           | :                           |     |
| Qy | 392 | AGIIVCPK     | KAANAGVA   | VSGL       | EMTQNR     | MSLWTR      | REVDRDKLERIKMDIVDSAMGSPRRV- | 450 |
|    |     | :            | :          | :          | :          | :           | :                           |     |
| Db | 360 | AGILYAPK     | ASNAGVAT   | SGLEMSQ    | NAITLSW    | TREEVORL    | PGIMQSHESCL-----KYG         | 415 |
|    |     | :            | :          | :          | :          | :           | :                           |     |
| Qy | 451 | ----         | NVDLAAG    | ANTAGTFK   | VADAVKAQ   | Q           | 474                         |     |
|    |     | :            | :          | :          | :          | :           | :                           |     |
| Db | 416 | KVGDTVNY     | VNGANTAG   | FKVKGAD    | AMLAAQ     | Q           | 443                         |     |
|    |     | :            | :          | :          | :          | :           | :                           |     |

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Job time : 94.9092 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 8, 2005, 02:10:48 ; Search time 91.1268 Seconds  
(without alignments)  
2104.671 Million cell updates/sec

Title: US-10-627-886-24

Perfect score: 2513

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Total number of hits satisfying chosen parameters: 1774312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query Match | ID                          | Description       |
|------------|--------|-------------|-----------------------------|-------------------|
| 1          | 2513   | 100.0       | 487 9 US-09-070-844-24      | Sequence 24, Appl |
| 2          | 2513   | 100.0       | 487 16 US-10-627-886-24     | Sequence 24, Appl |
| 3          | 2508   | 99.8        | 512 9 US-09-070-844-4       | Sequence 4, Appl  |
| 4          | 2508   | 99.8        | 512 16 US-10-627-886-4      | Sequence 4, Appl  |
| 5          | 2508   | 99.8        | 526 9 US-09-070-844-2       | Sequence 2, Appl  |
| 6          | 2508   | 99.8        | 526 16 US-10-627-886-2      | Sequence 2, Appl  |
| 7          | 2465   | 98.1        | 476 9 US-09-070-844-26      | Sequence 26, Appl |
| 8          | 2465   | 98.1        | 476 16 US-10-627-886-26     | Sequence 26, Appl |
| 9          | 1309   | 52.1        | 445 15 US-10-282-122A-66687 | Sequence 66687, A |
| 10         | 1300.5 | 51.8        | 444 18 US-10-988-943-43     | Sequence 43, Appl |
| 11         | 1297.5 | 51.6        | 444 15 US-10-282-122A-65129 | Sequence 65129, A |

|    |        |      |                             |                    |
|----|--------|------|-----------------------------|--------------------|
| 12 | 1294.5 | 51.5 | 444 15 US-10-282-122A-66041 | Sequence 66041, A  |
| 13 | 1294.5 | 51.5 | 444 15 US-10-275-026A-152   | Sequence 152, App  |
| 14 | 1287.5 | 51.2 | 449 15 US-10-282-122A-67538 | Sequence 67538, A  |
| 15 | 1281   | 51.0 | 445 15 US-10-369-493-13947  | Sequence 13947, A  |
| 16 | 1259   | 50.1 | 454 15 US-10-369-493-9839   | Sequence 9839, Ap  |
| 17 | 1257.5 | 50.0 | 462 15 US-10-282-122A-45200 | Sequence 45200, A  |
| 18 | 1239.5 | 49.3 | 448 15 US-10-282-122A-57310 | Sequence 57310, A  |
| 19 | 1239.5 | 49.3 | 448 18 US-10-953-901-338    | Sequence 338, App  |
| 20 | 1238   | 49.3 | 449 14 US-10-260-877-90     | Sequence 90, Appl  |
| 21 | 1238   | 49.3 | 449 15 US-10-282-122A-58096 | Sequence 58096, A  |
| 22 | 1230.5 | 48.0 | 449 15 US-10-282-122A-72329 | Sequence 72329, A  |
| 23 | 1230   | 48.9 | 449 15 US-10-282-122A-66870 | Sequence 66870, A  |
| 24 | 1214   | 48.3 | 448 15 US-10-282-122A-74024 | Sequence 74024, A  |
| 25 | 1212   | 48.2 | 448 17 US-10-472-928-2632   | Sequence 2632, App |
| 26 | 1211.5 | 48.2 | 448 18 US-10-953-901-340    | Sequence 340, App  |
| 27 | 1210.5 | 48.2 | 458 15 US-10-369-493-17284  | Sequence 17284, A  |
| 28 | 1207.5 | 48.1 | 464 15 US-10-282-122A-51278 | Sequence 51278, A  |
| 29 | 1205.5 | 48.0 | 424 15 US-10-369-493-617    | Sequence 617, App  |
| 30 | 1205.5 | 48.0 | 444 15 US-10-282-122A-48442 | Sequence 48442, A  |
| 31 | 1201   | 47.8 | 447 15 US-10-369-493-859    | Sequence 859, App  |
| 32 | 1201   | 47.8 | 447 15 US-10-282-122A-43284 | Sequence 43284, A  |
| 33 | 1199   | 47.7 | 443 15 US-10-282-122A-52117 | Sequence 52117, A  |
| 34 | 1196.5 | 47.6 | 456 15 US-10-425-114-72961  | Sequence 72961, A  |
| 35 | 1195.5 | 47.6 | 438 15 US-10-369-493-8215   | Sequence 8215, Ap  |
| 36 | 1194   | 47.5 | 438 15 US-10-369-493-10621  | Sequence 10621, A  |
| 37 | 1191   | 47.4 | 447 15 US-10-282-122A-60243 | Sequence 60243, A  |
| 38 | 1191   | 47.4 | 447 20 US-11-073-550-80     | Sequence 80, Appl  |
| 39 | 1185   | 47.2 | 447 9 US-09-738-626-6982    | Sequence 6982, Ap  |
| 40 | 1184   | 47.1 | 447 20 US-11-073-550-82     | Sequence 82, Appl  |
| 41 | 1182.5 | 47.1 | 448 15 US-10-282-122A-53998 | Sequence 53998, A  |
| 42 | 1181   | 47.0 | 447 15 US-10-282-122A-75593 | Sequence 75593, A  |
| 43 | 1180.5 | 47.0 | 458 15 US-10-282-122A-60810 | Sequence 60810, A  |
| 44 | 1180   | 47.0 | 447 15 US-10-369-493-295    | Sequence 295, App  |
| 45 | 1178   | 46.9 | 447 15 US-10-282-122A-72769 | Sequence 72769, A  |

#### ALIGNMENTS

RESULT 1  
US-09-070-844-24  
; Sequence 24, Application US/09070844  
; Patent No. US20020062495A1  
; GENERAL INFORMATION:  
; APPLICANT: Schmidt, Robert R.  
; APPLICANT: Miller, Philip  
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
; TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE  
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/09/070.844  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/725.596  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Whitlock, Ted W.  
; REGISTRATION NUMBER: 36,965  
; REFERENCE/DOCKET NUMBER: UF155

```
/ ; TELECOMMUNICATION INFORMATION:
/ ; TELEPHONE: (904) 375-8100
/ ; TELEFAX: (904) 372-5800
/ ; INFORMATION FOR SEQ ID NO: 24:
/ ; SEQUENCE CHARACTERISTICS:
/ ; LENGTH: 487 amino acids
/ ; TYPE: amino acid
/ ; TOPOLOGY: linear
/ ; MOLECULE TYPE: protein
/ ; US-09-070-844-24

Query Match      100.0%; Score 2513; DB 9; Length 487;
Best Local Similarity 100.0%; Pred. No. 3.9e-218;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 181 VNRFCQSPMTLQRHISYVDVPAGDIGVGAREIGYLPFGQYKRITKNTVGLTPKGQBYG 240
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DB 241 GSEIRPEATGYGAVLFVENVLKDKGESLKGKCLVSGAGNVAQYCAELLLKGAIVLSLS 300
QY 301 DSQGYVYEPNGFTREQLQAVQDMKKKNSARISEYKSDTAVVVGDRRKPWELDCQVDIAF 360
DB 301 DSQGYVYEPNGFTREQLQAVQDMKKKNSARISEYKSDTAVVVGDRRKPWELDCQVDIAF 360
QY 361 PCATQNEIDEHDAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIIPCPCGAANAGGVAV 420
DB 361 PCATQNEIDEHDAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIIPCPCGAANAGGVAV 420
QY 421 SGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRYNNVDLAAGANTAGFTKVADA 480
DB 421 SGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRYNNVDLAAGANTAGFTKVADA 480
QY 481 VKAQGAV 487
DB 481 VKAQGAV 487

RESULT 2
US-10-627-886-24
; Sequence 24, Application US/10627886
; Publication No. US20040128710A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
; DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606-6669
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

/ ; OPERATING SYSTEM: PC-DOS/MS-DOS
/ ; SOFTWARE: PatentIn Release #1.0, Version #1.25
/ ; CURRENT APPLICATION DATA:
/ ; APPLICATION NUMBER: US/10/627,886
/ ; FILING DATE: 24-Jul-2003
/ ; CLASSIFICATION: <Unknown>
/ ; PRIOR APPLICATION DATA:
/ ; APPLICATION NUMBER: 09/070,844
/ ; FILING DATE: 01-MAY-98
/ ; APPLICATION NUMBER: 08/725,596
/ ; FILING DATE: 03-OCT-96
/ ; APPLICATION NUMBER: 08/541,033
/ ; FILING DATE: 06-OCT-95
/ ; ATTORNEY/AGENT INFORMATION:
/ ; NAME: Lloyd, Jeff
/ ; REGISTRATION NUMBER: 35,589
/ ; REFERENCE/DOCKET NUMBER: UF-155CD3
/ ; TELECOMMUNICATION INFORMATION:
/ ; TELEPHONE: (352) 375-8100
/ ; TELEFAX: (352) 372-5800
/ ; INFORMATION FOR SEQ ID NO: 24:
/ ; SEQUENCE CHARACTERISTICS:
/ ; LENGTH: 487 amino acids
/ ; TYPE: amino acid
/ ; TOPOLOGY: linear
/ ; MOLECULE TYPE: protein
/ ; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
/ ; US-10-627-886-24

Query Match      100.0%; Score 2513; DB 16; Length 487;
Best Local Similarity 100.0%; Pred. No. 3.9e-218;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAVSLEEQISAMDATGDTALQKAVQMATKAGTEGLVHGIKNPDVRLQLLTFPMKDPE 60
DB 1 MAVSLEEQISAMDATGDTALQKAVQMATKAGTEGLVHGIKNPDVRLQLLTFPMKDPE 60
QY 61 QOEFMQAVREAVSLQPVFEKPELLPIFKQIVPEPVIITFRVSWLDDAGNLQVNRGRV 120
DB 61 QOEFMQAVREAVSLQPVFEKPELLPIFKQIVPEPVIITFRVSWLDDAGNLQVNRGRV 120
QY 121 QYSSAIGPYKGLRPHPSVNLISIMKFLAFAQEIQFKNSLTTLPMGGGKGGSDPDKGKSDAE 180
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DB 421 SGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRYNNVDLAAGANTAGFTKVADA 480
QY 481 VKAQGAV 487
DB 481 VKAQGAV 487

RESULT 3
US-09-070-844-4
; Sequence 4, Application US/09070844
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Patent No. US20020062495A1  
GENERAL INFORMATION:  
APPLICANT: Schmidt, Robert R.  
APPLICANT: Miller, Philip  
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE  
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: US/09/070,844  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/725,596  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Whitlock, Ted W.  
REGISTRATION NUMBER: 36,965  
REFERENCE/DOCKET NUMBER: UF155  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 512 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-070-844-4  
Query Match 99.8%; Score 2508; DB 9; Length 512;  
Best Local Similarity 100.0%; Pred. No. 1.2e-217;  
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 AVSLEEQISAMDATGDFALQKAVKQMATKAGTEGLVHGINKNPDVQRQLLTETIFMKDPEQ 61  
DB 27 AVSLEEQISAMDATGDFALQKAVKQMATKAGTEGLVHGINKNPDVQRQLLTETIFMKDPEQ 86  
QY 62 QEFMQAVREVAVSLQVPFEKRPPELLPIFKQIVPEPVTITFRVSWLDDAGNLQVNRGFRVQ 121  
DB 87 QEFMQAVREVAVSLQVPFEKRPPELLPIFKQIVPEPVTITFRVSWLDDAGNLQVNRGFRVQ 146  
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QY 482 KQAGAV 487  
DB 507 KQAGAV 512  
RESULT 4  
US-10-627-886-4  
Sequence 4, Application US/10627886  
Publication No. US20040128710A1  
GENERAL INFORMATION:  
APPLICANT: Schmidt, Robert R.  
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE  
DEHYDROGENASES AND METHODS OF USE  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
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STATE: Florida  
COUNTRY: USA  
ZIP: 32606-6669  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/627,886  
FILING DATE: 24-Jul-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/070,844  
FILING DATE: 01-MAY-98  
APPLICATION NUMBER: 08/725,596  
FILING DATE: 03-OCT-96  
APPLICATION NUMBER: 08/541,033  
FILING DATE: 06-OCT-95  
ATTORNEY/AGENT INFORMATION:  
NAME: Lloyd, Jeff  
REGISTRATION NUMBER: 35,589  
REFERENCE/DOCKET NUMBER: UF-155CD3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (352) 375-8100  
TELEFAX: (352) 372-5800  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 512 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-10-627-886-4  
Query Match 99.8%; Score 2508; DB 16; Length 512;  
Best Local Similarity 100.0%; Pred. No. 1.2e-217;  
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 27 AVSLEEQISAMDATGDFALQKAVKQMATKAGTEGLVHGINKNPDVQRQLLTETIFMKDPEQ 86  
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QY 242 SEIRPEATGYGAVLFVENVLKDKGSLKGRCLVSGAGNVAQYCAELILEKGAIVLSLSD 301  
Db 267 SEIRPEATGYGAVLFVENVLKDKGSLKGRCLVSGAGNVAQYCAELILEKGAIVLSLSD 326  
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QY 422 GLEMTQNRMSLNWTREEVDRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAV 481  
Db 447 GLEMTQNRMSLNWTREEVDRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAV 506  
QY 482 KAQNAV 487  
Db 507 KAQNAV 512

## RESULT 5

US-09-070-844-2  
; Sequence 2, Application US/09070844  
; Patent No. US20020062495A1  
; GENERAL INFORMATION:  
; APPLICANT: Schmidt, Robert R.  
; APPLICANT: Miller, Philip  
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
; TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE  
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/070,844  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/725,596  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Whitlock, Ted W.  
; REGISTRATION NUMBER: 36,965  
; REFERENCE/DOCKET NUMBER: UF155  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (904) 375-8100  
; TELEFAX: (904) 372-5800  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 526 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-070-844-2

Query Match 99.8%; Score 2508; DB 9; Length 526;  
Best Local Similarity 100.0%; Pred. No. 1.2e-217; Indels 0; Gaps 0;  
Matches 486; Conservative 0; Mismatches 0;  
QY 2 AVSLEEQISAMDAITTDGFTALQKAVQMATKAGTEGLVHGKIPNDVROLLEIFMKDPEQ 61  
Db 41 AVSLEEQISAMDAITTDGFTALQKAVQMATKAGTEGLVHGKIPNDVROLLEIFMKDPEQ 100  
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QY 242 SEIRPEATGYGAVLFVENVLKDKGSLKGRCLVSGAGNVAQYCAELILEKGAIVLSLSD 301  
Db 281 SEIRPEATGYGAVLFVENVLKDKGSLKGRCLVSGAGNVAQYCAELILEKGAIVLSLSD 340  
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## RESULT 6

US-10-627-886-2  
; Sequence 2, Application US/10627886  
; Publication No. US20040128710A1  
; GENERAL INFORMATION:  
; APPLICANT: Schmidt, Robert R.  
; APPLICANT: Miller, Philip  
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
; RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE  
; DEHYDROGENASES AND METHODS OF USE  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606-6669  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/627,886  
; FILING DATE: 24-Jul-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/070,844  
; FILING DATE: 01-MAY-98  
; APPLICATION NUMBER: 08/725,596  
; FILING DATE: 03-OCT-96

APPLICATION NUMBER: 08/541,033  
FILING DATE: 06-OCT-95  
ATTORNEY/AGENT INFORMATION:  
NAME: Lloyd, Jeff  
REGISTRATION NUMBER: 35,589  
REFERENCE/DOCKET NUMBER: UF-155CD3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (352) 375-8100  
TELEFAX: (352) 372-5800  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 526 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-627-886-2

Query Match 99.8%; Score 2508; DB 16; Length 526;  
Best Local Similarity 100.0%; Pred. No. 1.2e-217;  
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AVSLEQISAMDATTCGDTALQAVKQMATKAGTEGLVHGINKPDPVRLTTEIFMKDPQ 61  
DB 41 AVSLEQISAMDATTCGDTALQAVKQMATKAGTEGLVHGINKPDPVRLTTEIFMKDPQ 100  
QY 62 QEFMQAVREAVSLQVPFEKRPPELLPIFKQIIVEPERVITFRVSWLDDAGNLQVNRGRVQ 121  
DB 101 QEFMQAVREAVSLQVPFEKRPPELLPIFKQIIVEPERVITFRVSWLDDAGNLQVNRGRVQ 160  
QY 122 YSAIGPYGGLRPHPSVNLISIMKFLAPQIFKNSLTTLPMGGGKGSDFDPKGSDAEV 181  
DB 161 YSAIGPYGGLRPHPSVNLISIMKFLAPQIFKNSLTTLPMGGGKGSDFDPKGSDAEV 220  
QY 182 MFCOSFMTLQRLHISYQDVDPAGDIGVAREIGYLFQYKRTKNTYTGVLTPKGOEYGG 241  
DB 221 MFCOSFMTLQRLHISYQDVDPAGDIGVAREIGYLFQYKRTKNTYTGVLTPKGOEYGG 280  
QY 242 SEIRPEATGYGAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSD 301  
DB 281 SEIRPEATGYGAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSD 340  
QY 302 SQGYVPEPFTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAPP 361  
DB 341 SQGYVPEPFTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAPP 400  
QY 362 CATONEIDSHDAELLIKHCQYVVEGANMPSTNEAIHKYNKAGIICPCGAANAGVAVS 421  
DB 401 CATONEIDSHDAELLIKHCQYVVEGANMPSTNEAIHKYNKAGIICPCGAANAGVAVS 460  
QY 422 GLEMTQNRMSLNTREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAV 481  
DB 461 GLEMTQNRMSLNTREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAV 520  
QY 482 KAQAV 487  
DB 521 KAQAV 526

RESULT 7  
US-09-070-844-26  
Sequence 26, Application US/09070844  
Patent No. US20020062495A1  
GENERAL INFORMATION:  
APPLICANT: Schmidt, Robert R.  
APPLICANT: Miller, Philip  
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE  
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/070,844  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/725,596  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Whitlock, Ted W.  
REGISTRATION NUMBER: 36,965  
REFERENCE/DOCKET NUMBER: UF155  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 476 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-070-844-26

Query Match 98.1%; Score 2465; DB 9; Length 476;  
Best Local Similarity 100.0%; Pred. No. 8.3e-214;  
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 MDATTGDTALQAVKQMATKAGTEGLVHGINKPDPVRLTTEIFMKDPQBFMQAVREV 71  
DB 1 MDATTGDTALQAVKQMATKAGTEGLVHGINKPDPVRLTTEIFMKDPQBFMQAVREV 60  
QY 72 AVSLOPVEKRPPELLPIFKQIIVEPERVITFRVSWLDDAGNLQVNRGRVVOYSSAIGPYKG 131  
DB 61 AVSLOPVEKRPPELLPIFKQIIVEPERVITFRVSWLDDAGNLQVNRGRVVOYSSAIGPYKG 120  
QY 132 GLRPHPSVNLISIMKFLAPEQIFKNSLTTLPMGGGKGSDFDPKGSDAEVMFQCOSFMTIE 191  
DB 121 GLRPHPSVNLISIMKFLAPEQIFKNSLTTLPMGGGKGSDFDPKGSDAEVMFQCOSFMTIE 180  
QY 192 LQRHISYQDVDPAGDIGVAREIGYLFQYKRTKNTYTGVLTPKGOEYGGSEIRPEATGY 251  
DB 181 LQRHISYQDVDPAGDIGVAREIGYLFQYKRTKNTYTGVLTPKGOEYGGSEIRPEATGY 240  
QY 252 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVPEPNG 311  
DB 241 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVPEPNG 300  
QY 312 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAPPQATQNEIDSH 371  
DB 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAPPQATQNEIDSH 360  
QY 372 DAELLIKHGCGYVVEGANMPSTNEAIHKYNKAGIICPCGAANAGVAVSGLSEMTQNRMS 431  
DB 361 DAELLIKHGCGYVVEGANMPSTNEAIHKYNKAGIICPCGAANAGVAVSGLSEMTQNRMS 420  
QY 432 LNTWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQAV 487  
DB 421 LNTWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQAV 476

RESULT 8  
US-10-627-886-26  
Sequence 26, Application US/10627886  
Publication No. US20040128710A1  
GENERAL INFORMATION:



Db 125 GKGSDPDPKGSDAEVRMFCQSPMSLYRHVGADLDVDPAGDIGVGAREIGYILFGQYKRL 184  
QY 225 TKNYTVGLTPKQGYGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCCLVSGAGNVAQY 284  
Db 185 SNQFTSVLTGKLSYGSLRPEATGCGYVFAQEMLKDRGRFDGQGVVAISGNNVAQY 244  
QY 285 CAELLLKGAIVLSLSDSQGYVVPNGFTFEQQLQAVQDMKKNNARSISEYKSDTAVYVG 344  
Db 245 AARKVMEGKGVLSLSDSEGTLYAEAGLSDEQWEYLMELKNVRR-GRIREMAEQFSLOFL 303  
QY 345 DRKPEWELDCQVDIAFPACATONEIDEHDAELLIKHGQYVVEGANMPSTNEATHKNKAG 404  
Db 304 EGRRPWGLAC--DIAUFPACATONELDAEDARRLLANGCVCVAEGANMPSTLEAVDLFLEAG 361  
QY 405 ILYCPGKAANAGGVAVSGLSMTQNRMSLNWTRREVRDKLERIMKDIYDSA-MGFSRRYV 463  
Db 362 ILVAPGKASAGGVAVSGLSMTQNRMSLNWTRREVRDKLERIMKDIYDSA-MGFSRRYV 463  
QY 464 DLAAAGNIAGFTKVADAVKAQGV 487  
Db 422 NYVKGANIAGFVKVADAMLAQGVV 445

RESULT 10  
US-10-988-943-43  
; Sequence 43, Application US/10988943  
; Publication No. US20050176085A1  
; GENERAL INFORMATION:  
; APPLICANT: Center for Genetic Engineering and Biotechnology  
; TITLE OF INVENTION: METHOD OF SELECTIVE PEPTIDE ISOLATION FOR THE  
; TITLE OF INVENTION: IDENTIFICATION AND QUANTITATIVE ANALYSIS OF PROTEINS IN  
; TITLE OF INVENTION: COMPLEX MIXTURES.  
; FILE REFERENCE: Proteomics CU2003-269  
; CURRENT APPLICATION NUMBER: US/10/988,943  
; CURRENT FILING DATE: 2004-11-15  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 43  
; LENGTH: 444  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis (group B)  
US-10-988-943-43

Query Match 51.8%; Score 1300.5; DB 18; Length 444;  
Best Local Similarity 57.4%; Pred. No. 1.6e-108;  
Matches 257; Conservative 72; Mismatches 104; Indels 15; Gaps 6;

QY 46 DVRQLLTFIMKDPQEQBFMQAVREAVSLQPVFEKRPPELL--PIPKQIVEPERVITFRV 103  
Db 3 DLNLTFLANLKQRPNPQEPFHQAEEVFMSLDPLAKNPKYTOQSLLERIVEPERVVMFRV 62

QY 104 SWLDDAGNLQVNRGFRVQYSSAIGPYKGLRHPHSVNLSIMKFLAEPQIFKNSLTPLMG 163  
Db 63 TWQDDRGQVQNRGFRVQYSSAIGPYKGLRHPHSVNLSIMKFLAEPQIFKNSLTPLMG 122

QY 164 GKGSDPDPKGSDAEVRMFCQSPMSLYRHVGADLDVDPAGDIGVGAREIGYILFGQYKRL 223  
Db 123 GKGSDPDPKGSDAEVRMFCQSPMSLYRHVGADLDVDPAGDIGVGAREIGYILFGQYKRL 182

QY 224 ITKNYTVGLTPKQGYGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCCLVSGAGNVAQ 283  
Db 183 IRNEFSSVLTGKLSYGSLRPEATGCGYVFAQEMLKDRGRFDGQGVVAISGNNVAQ 242

QY 284 YCAELLLKGAIVLSLSDSQGYVVPNGFTFEQQLQAVQDMKKNNARSISEYKSDTAVYVG 344  
Db 243 YAAEKAIQLGAKVLTVDSDNGFVLPDSDGTEAQLAALIELKEVRRE-RVATYAKEQGLQ 301

QY 343 VGDRRKPEWELDCQVDIAFPACATONEIDEHDAELLIKHGQYVVEGANMPSTNEATHKNK 402  
Db 302 YFEKQKPMGV--AAETALPACATONELDEAAKTLANGCVCVAEGANMPSTLEAVDLFLEAG 361

QY 403 AGIYCPGKAANAGGVAVSGLSMTQNRMSLNWTRREVRDKLERIMKDIYDSANGFSRRY- 461  
Db 422 NYVKGANIAGFVKVADAMLAQGVV 445

Db 360 AGIYAPGKASAGGVAVSGLSMTQNRMSLNWTRREVRDKLERIMKDIYDSANGFSRRY- 461  
QY 462 ----NYDLAAGNIAGFTKVADAVKAQGV 485  
Db 416 KVGDTVNYVNGANIAGFVKVADAMLAQGV 443

RESULT 11  
US-10-282-122A-65129  
; Sequence 65129, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Karl  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Cart, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA 034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 65129  
; LENGTH: 444  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-282-122A-65129

Query Match 51.6%; Score 1297.5; DB 15; Length 444;  
Best Local Similarity 57.4%; Pred. No. 3e-108;  
Matches 257; Conservative 70; Mismatches 106; Indels 15; Gaps 6;

QY 46 DVRQLLTFIMKDPQEQBFMQAVREAVSLQPVFEKRPPELL--PIPKQIVEPERVITFRV 103  
Db 3 DLNLTFLANLKQRPNPQEPFHQAEEVFMSLDPLAKNPKYTOQSLLERIVEPERVVMFRV 62

QY 104 SWLDDAGNLQVNRGFRVQYSSAIGPYKGLRHPHSVNLSIMKFLAEPQIFKNSLTPLMG 163  
Db 63 TWQDDRGQVQNRGFRVQYSSAIGPYKGLRHPHSVNLSIMKFLAEPQIFKNSLTPLMG 122

QY 164 GKGSDPDPKGSDAEVRMFCQSPMSLYRHVGADLDVDPAGDIGVGAREIGYILFGQYKRL 223  
Db 123 GKGSDPDPKGSDAEVRMFCQSPMSLYRHVGADLDVDPAGDIGVGAREIGYILFGQYKRL 182

QY 224 ITKNVTGVLTPKQEGYSGSEIRPEATGYGAVLFVENVLKDKGSLKGRCLVSGAGNVAQ 283  
DB 183 INRETSVLTGKLEWGGSLIRPEATGYCVYFAQAMLQTRNDSPEGKRVLSGSGNVAQ 242  
QY 284 YCAELLEKGAIVLSLSDSQGYVYBPN-GFTREQLQAVQDMKKKNSARISEYKSDTAVY 342  
DB 243 YAAEKAIQIGAKVLTIVSDSDGFVLPDIDGWTQAQLAALIELKEVRRE-RVATYAKEQGLQ 301  
QY 343 VGDRRKPWELDCQVDIAFFCATQNEIDHDAELLIKHGCQYVVEGANMPSTNEATHKYNK 402  
DB 302 YFENQKPMGV--AAEIALPCATQNELDEBAKTLANGCYVVAEGANMPSTLGAVEQFIK 359  
QY 403 AGIITYCPGKAANAGGVAVSGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRY- 461  
DB 360 AGIITYAPGKASNAGGVATSGLEMSQNAIRLSWTRREVRDQLRFGIMQSIHESCL----KYG 415  
QY 462 ----NVDLAAGANAGFTTKVADAVKAQ 485  
DB 416 KVGDKVNYVNGANIAGFVKVADAMLAQ 443

## RESULT 12

US-10-282-122A-66041  
; Sequence 66041, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 66041  
; LENGTH: 444  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis

Query Match 51.5%; Score 1294.5; DB 15; Length 444;

Best Local Similarity 57.1%; Pred. No. 5.7e-108;

Matches 256; Conservative 72; Mismatches 105; Indels 15; Gaps 6;

QY 46 DVRLQLTIFMKDPEQEFMQAVREVAVSLQVFEKRPPELL--PIFKOIVPERVITPRV 103

DB 3 DLNTLFAULKORNPQEPFHQAVEVFMSLDPPFLAKNPYTKQSSLERIVERPVMRPRV 62

QY 104 SWLDDAGNLQVNRGRFVQYSSAIGPYKGLRPHSPVNSIMKFLAFEOIFKNSLTTLPMG 163

DB 63 TWQDDKGGQVNRGRYRVQMSAIGPYKGLRPHSPVNSIMKFLAFEOIFKNSLTTLPMG 122

QY 164 GKGSGDFDPKGSDAEVMRFQCSFMTLORHISYVQVDPAGDIGVGAREIGYLFQGYKR 223

DB 123 GKGSGDFDPKGSDAEVMRFQCSFMTLORHISYVQVDPAGDIGVGAREIGYLFQGYKR 182

Query Match 51.5%; Score 1294.5; DB 15; Length 444;

Best Local Similarity 57.1%; Pred. No. 5.7e-108;

Matches 256; Conservative 72; Mismatches 105; Indels 15; Gaps 6;

Matches 256; Conservative 72; Mismatches 105; Indels 15; Gaps 6;  
QY 46 DVRLQLTIFMKDPEQEFMQAVREVAVSLQVFEKRPPELL--PIFKOIVPERVITPRV 103  
DB 3 DLNTLFAULKORNPQEPFHQAVEVFMSLDPPFLAKNPYTKQSSLERIVERPVMRPRV 62  
QY 104 SWLDDAGNLQVNRGRFVQYSSAIGPYKGLRPHSPVNSIMKFLAFEOIFKNSLTTLPMG 163  
DB 63 TWQDDKGGQVNRGRYRVQMSAIGPYKGLRPHSPVNSIMKFLAFEOIFKNSLTTLPMG 122  
QY 164 GKGSGDFDPKGSDAEVMRFQCSFMTLORHISYVQVDPAGDIGVGAREIGYLFQGYKR 223  
DB 123 GKGSGDFDPKGSDAEVMRFQCSFMTLORHISYVQVDPAGDIGVGAREIGYLFQGYKR 182  
QY 224 ITKNVTGVLTPKQEGYSGSEIRPEATGYGAVLFVENVLKDKGSLKGRCLVSGAGNVAQ 283  
DB 183 INRETSVLTGKLEWGGSLIRPEATGYCVYFAQAMLQTRNDSPEGKRVLSGSGNVAQ 242  
QY 284 YCAELLEKGAIVLSLSDSQGYVYBPN-GFTREQLQAVQDMKKKNSARISEYKSDTAVY 342  
DB 243 YAAEKAIQIGAKVLTIVSDSDGFVLPDIDGWTQAQLAALIELKEVRRE-RVATYAKEQGLQ 301  
QY 343 VGDRRKPWELDCQVDIAFFCATQNEIDHDAELLIKHGCQYVVEGANMPSTNEATHKYNK 402  
DB 302 YFENQKPMGV--AAEIALPCATQNELDEBAKTLANGCYVVAEGANMPSTLGAVEQFIK 359  
QY 403 AGIITYCPGKAANAGGVAVSGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRY- 461  
DB 360 AGIITYAPGKASNAGGVATSGLEMSQNAIRLSWTRREVRDQLRFGIMQSIHESCL----KYG 415  
QY 462 ----NVDLAAGANAGFTTKVADAVKAQ 485  
DB 416 KVGDKVNYVNGANIAGFVKVADAMLAQ 443

## RESULT 13

US-10-275-026A-152  
; Sequence 152, Application US/10275026A  
; Publication No. US2004008770A1  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Christoph  
; TITLE OF INVENTION: Virulence Genes, Proteins, and Their Use  
; FILE REFERENCE: GJE-6436  
; CURRENT APPLICATION NUMBER: US/10/275,026A  
; CURRENT FILING DATE: 2003-10-31  
; PRIOR APPLICATION NUMBER: PCT/GB01/02003  
; PRIOR FILING DATE: 2001-05-08  
; PRIOR APPLICATION NUMBER: GB 0011108.8  
; PRIOR FILING DATE: 2000-05-08  
; NUMBER OF SEQ ID NOS: 214  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 152  
; LENGTH: 444  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-10-275-026A-152

Query Match 51.5%; Score 1294.5; DB 15; Length 444;

Best Local Similarity 57.1%; Pred. No. 5.7e-108;

Matches 256; Conservative 72; Mismatches 105; Indels 15; Gaps 6;

QY 46 DVRLQLTIFMKDPEQEFMQAVREVAVSLQVFEKRPPELL--PIFKOIVPERVITPRV 103

DB 3 DLNTLFAULKORNPQEPFHQAVEVFMSLDPPFLAKNPYTKQSSLERIVERPVMRPRV 62

QY 104 SWLDDAGNLQVNRGRFVQYSSAIGPYKGLRPHSPVNSIMKFLAFEOIFKNSLTTLPMG 163

DB 63 TWQDDKGGQVNRGRYRVQMSAIGPYKGLRPHSPVNSIMKFLAFEOIFKNSLTTLPMG 122

QY 164 GKGSGDFDPKGSDAEVMRFQCSFMTLORHISYVQVDPAGDIGVGAREIGYLFQGYKR 223

DB 123 GKGSGDFDPKGSDAEVMRFQCSFMTLORHISYVQVDPAGDIGVGAREIGYLFQGYKR 182







| Result No. | Query  |       |        | DB | ID                   | Description       |
|------------|--------|-------|--------|----|----------------------|-------------------|
|            | Score  | Match | Length |    |                      |                   |
| 1          | 2513   | 100.0 | 487    | 2  | US-08-541-033A-24    | Sequence 24, Appl |
| 2          | 2513   | 100.0 | 487    | 2  | US-08-828-451-24     | Sequence 24, Appl |
| 3          | 2508   | 99.8  | 512    | 2  | US-08-541-033A-4     | Sequence 4, Appl  |
| 4          | 2508   | 99.8  | 512    | 2  | US-08-828-451-4      | Sequence 4, Appl  |
| 5          | 2508   | 99.8  | 526    | 2  | US-08-541-033A-2     | Sequence 2, Appl  |
| 6          | 2508   | 99.8  | 526    | 2  | US-08-828-451-2      | Sequence 2, Appl  |
| 7          | 2465   | 98.1  | 476    | 2  | US-08-541-033A-26    | Sequence 26, Appl |
| 8          | 2465   | 98.1  | 476    | 2  | US-08-828-451-26     | Sequence 26, Appl |
| 9          | 1309   | 52.1  | 450    | 4  | US-09-252-991A-20646 | Sequence 20646, A |
| 10         | 1257.5 | 50.0  | 467    | 4  | US-09-328-352-5725   | Sequence 5725, Ap |
| 11         | 1234.5 | 49.1  | 448    | 4  | US-09-134-000C-3884  | Sequence 3884, Ap |
| 12         | 1221   | 48.6  | 448    | 4  | US-09-583-110-4489   | Sequence 4489, Ap |
| 13         | 1201   | 47.8  | 447    | 2  | US-08-886-640-3      | Sequence 3, Appl  |
| 14         | 1201   | 47.8  | 447    | 3  | US-08-884-235-11     | Sequence 11, Appl |
| 15         | 1200   | 47.8  | 447    | 1  | US-08-370-193A-11    | Sequence 11, Appl |
| 16         | 1191   | 47.4  | 452    | 4  | US-09-489-039A-7937  | Sequence 7937, Ap |
| 17         | 1177.5 | 46.9  | 446    | 4  | US-09-543-681A-6657  | Sequence 6657, Ap |
| 18         | 1177   | 46.8  | 447    | 3  | US-08-508-761B-6     | Sequence 6, Appl  |
| 19         | 1147   | 45.6  | 461    | 3  | US-09-171-337A-5     | Sequence 5, Appl  |
| 20         | 1147   | 45.6  | 461    | 4  | US-09-631-022-5      | Sequence 5, Appl  |
| 21         | 1143   | 45.5  | 449    | 1  | US-08-831-753-1      | Sequence 1, Appl  |
| 22         | 1037.5 | 41.3  | 454    | 4  | US-09-538-092-767    | Sequence 767, App |
| 23         | 1012   | 40.3  | 368    | 4  | US-09-107-433-4041   | Sequence 4041, Ap |
| 24         | 788.5  | 31.4  | 298    | 4  | US-09-248-798A-17483 | Sequence 17483, A |
| 25         | 552.5  | 22.0  | 420    | 3  | US-09-134-001C-3103  | Sequence 3103, Ap |
| 26         | 537.5  | 21.4  | 374    | 4  | US-09-710-279-2162   | Sequence 2162, Ap |
| 27         | 537    | 21.4  | 509    | 4  | US-09-902-540-11352  | Sequence 11352, A |

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QY 61 QQEFMQAVREAVSLQPVFEKPELLPIFKQIVPEPVTFRVSWLDDAGNLQVNRGRV 120
DB 61 QQEFMQAVREAVSLQPVFEKPELLPIFKQIVPEPVTFRVSWLDDAGNLQVNRGRV 120
QY 121 QYSSAIGPYKGLRPHPSVNLISIMKFLAPEQIFKNSLTTLPMGGGKGSDFDPKGSDAE 180
DB 121 QYSSAIGPYKGLRPHPSVNLISIMKFLAPEQIFKNSLTTLPMGGGKGSDFDPKGSDAE 180
QY 181 VMRFQCSFMTLQRHISYVQDVDPAGDIGVAREIGYLFQGYKRITKNTYTVGLTPKGQBYG 240
DB 181 VMRFQCSFMTLQRHISYVQDVDPAGDIGVAREIGYLFQGYKRITKNTYTVGLTPKGQBYG 240
QY 241 GSEIRPEATGYGAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLKGAIVLSLS 300
DB 241 GSEIRPEATGYGAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLKGAIVLSLS 300
QY 301 DSQGYVYEPNGFTREQLQAVQDMKKNSARISEYKSDTAVYVGDRRKPEWELDCQVDIAF 360
DB 301 DSQGYVYEPNGFTREQLQAVQDMKKNSARISEYKSDTAVYVGDRRKPEWELDCQVDIAF 360
QY 361 PCATONEIDEHDAELLIKHGCOYVVEGANMPSTNEAIIHKYNKAGIICPGKAANAGGVAV 420
DB 361 PCATONEIDEHDAELLIKHGCOYVVEGANMPSTNEAIIHKYNKAGIICPGKAANAGGVAV 420
QY 421 SGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANTAGFTKVADA 480
DB 421 SGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANTAGFTKVADA 480
QY 481 VKAQAV 487
DB 481 VKAQAV 487
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## RESULT 2

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US-08-828-451-24
; Sequence 24, Application US/08828451
; Patent No. 5985634
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,451
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,033
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UFI15
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-828-451-24
Query Match 100.0%; Score 2513; DB 2; Length 487;
Best Local Similarity 100.0%; Pred. No. 4,1e-223;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAVSLEEQISAMDATTTGDTALQKAVQMATKAGTEGLVHGINKPDPVRLQLTEIFMKDPE 60
DB 1 MAVSLEEQISAMDATTTGDTALQKAVQMATKAGTEGLVHGINKPDPVRLQLTEIFMKDPE 60
QY 61 QQEFMQAVREAVSLQPVFEKPELLPIFKQIVPEPVTFRVSWLDDAGNLQVNRGRV 120
DB 61 QQEFMQAVREAVSLQPVFEKPELLPIFKQIVPEPVTFRVSWLDDAGNLQVNRGRV 120
QY 121 QYSSAIGPYKGLRPHPSVNLISIMKFLAPEQIFKNSLTTLPMGGGKGSDFDPKGSDAE 180
DB 121 QYSSAIGPYKGLRPHPSVNLISIMKFLAPEQIFKNSLTTLPMGGGKGSDFDPKGSDAE 180
QY 181 VMRFQCSFMTLQRHISYVQDVDPAGDIGVAREIGYLFQGYKRITKNTYTVGLTPKGQBYG 240
DB 181 VMRFQCSFMTLQRHISYVQDVDPAGDIGVAREIGYLFQGYKRITKNTYTVGLTPKGQBYG 240
QY 241 GSEIRPEATGYGAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLKGAIVLSLS 300
DB 241 GSEIRPEATGYGAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLKGAIVLSLS 300
QY 301 DSQGYVYEPNGFTREQLQAVQDMKKNSARISEYKSDTAVYVGDRRKPEWELDCQVDIAF 360
DB 301 DSQGYVYEPNGFTREQLQAVQDMKKNSARISEYKSDTAVYVGDRRKPEWELDCQVDIAF 360
QY 361 PCATONEIDEHDAELLIKHGCOYVVEGANMPSTNEAIIHKYNKAGIICPGKAANAGGVAV 420
DB 361 PCATONEIDEHDAELLIKHGCOYVVEGANMPSTNEAIIHKYNKAGIICPGKAANAGGVAV 420
QY 421 SGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANTAGFTKVADA 480
DB 421 SGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANTAGFTKVADA 480
QY 481 VKAQAV 487
DB 481 VKAQAV 487
RESULT 3
US-08-541-033A-4
; Sequence 4, Application US/08541033A
; Patent No. 5879941
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,033A
; FILING DATE:
; CLASSIFICATION: 435
```

## ATTORNEY/AGENT INFORMATION:

NAME: Whitlock, Ted W.  
REGISTRATION NUMBER: 36,965  
REFERENCE/DOCKET NUMBER: UF155  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 512 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-541-033A-4

Query Match 99.8%; Score 2508; DB 2; Length 512;  
Best Local Similarity 100.0%; Pred. No. 1.3e-222;  
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AVSLEQISAMDTTGDFTALQKAVKQMATKAGTEGLVHGINKPDRVRLQLTEIFMKDPEQ 61  
Db |  
QY 27 AVSLEQISAMDTTGDFTALQKAVKQMATKAGTEGLVHGINKPDRVRLQLTEIFMKDPEQ 86  
Db |  
QY 62 QEFMQAVREAVSLQPVFEKRPPELLPIFKQIVPEPVIITFRVSWLDDAGNLQVNRGRVQ 121  
Db |  
QY 87 QEFMQAVREAVSLQPVFEKRPPELLPIFKQIVPEPVIITFRVSWLDDAGNLQVNRGRVQ 146  
Db |  
QY 122 YSSAIGPYKGLRPHSPVNLISIMKFLAFQIFKNSLTTLPMGGGKGSDFDPKGSDAEV 181  
Db |  
QY 147 YSSAIGPYKGLRPHSPVNLISIMKFLAFQIFKNSLTTLPMGGGKGSDFDPKGSDAEV 206  
Db |  
QY 182 MRFQCSFMTLQRLHSYVQDPVAGDIGVGAREIGYLFQYKRTKNTYGVLTLPKGQYGG 241  
Db |  
QY 207 MRFQCSFMTLQRLHSYVQDPVAGDIGVGAREIGYLFQYKRTKNTYGVLTLPKGQYGG 266  
Db |  
QY 242 SEIRPEATGYGAVLFVENVLKDGSLSKRCCLVSGAGNVAQYCAELLEKGAIIVLSLD 301  
Db |  
QY 267 SEIRPEATGYGAVLFVENVLKDGSLSKRCCLVSGAGNVAQYCAELLEKGAIIVLSLD 326  
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QY 302 SQGYVPEPNGFTREQLQAVQDMKKNSARISEYKSDTAVYVGDRLKRWELDCQVDIAPP 361  
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QY 362 CATONEIDEHDAELLIKHGQYVVEGANPSTNEAIHKYNKAGIYICPGKAANAGGVAVS 421  
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QY 387 CATONEIDEHDAELLIKHGQYVVEGANPSTNEAIHKYNKAGIYICPGKAANAGGVAVS 446  
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QY 422 GLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVVADAV 481  
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QY 447 GLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVVADAV 506  
Db |  
QY 482 KAQGA 487  
Db |  
QY 507 KAQGA 512

## RESULT 4

US-08-541-033A-4  
Sequence 4, Application US/08028451  
Patent No. 5985634

## GENERAL INFORMATION:

APPLICANT: Schmidt, Robert R.  
APPLICANT: Miller, Philip  
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE  
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA

ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/828,451  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/541,033  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Whitlock, Ted W.  
REGISTRATION NUMBER: 36,965  
REFERENCE/DOCKET NUMBER: UF155  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 512 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-828-451-4

Query Match 99.8%; Score 2508; DB 2; Length 512;  
Best Local Similarity 100.0%; Pred. No. 1.3e-222;  
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AVSLEQISAMDTTGDFTALQKAVKQMATKAGTEGLVHGINKPDRVRLQLTEIFMKDPEQ 61  
Db |  
QY 27 AVSLEQISAMDTTGDFTALQKAVKQMATKAGTEGLVHGINKPDRVRLQLTEIFMKDPEQ 86  
Db |  
QY 62 QEFMQAVREAVSLQPVFEKRPPELLPIFKQIVPEPVIITFRVSWLDDAGNLQVNRGRVQ 121  
Db |  
QY 87 QEFMQAVREAVSLQPVFEKRPPELLPIFKQIVPEPVIITFRVSWLDDAGNLQVNRGRVQ 146  
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QY 147 YSSAIGPYKGLRPHSPVNLISIMKFLAFQIFKNSLTTLPMGGGKGSDFDPKGSDAEV 206  
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QY 182 MRFQCSFMTLQRLHSYVQDPVAGDIGVGAREIGYLFQYKRTKNTYGVLTLPKGQYGG 241  
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QY 207 MRFQCSFMTLQRLHSYVQDPVAGDIGVGAREIGYLFQYKRTKNTYGVLTLPKGQYGG 266  
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QY 327 SQGYVPEPNGFTREQLQAVQDMKKNSARISEYKSDTAVYVGDRLKRWELDCQVDIAPP 386  
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QY 362 CATONEIDEHDAELLIKHGQYVVEGANPSTNEAIHKYNKAGIYICPGKAANAGGVAVS 421  
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QY 387 CATONEIDEHDAELLIKHGQYVVEGANPSTNEAIHKYNKAGIYICPGKAANAGGVAVS 446  
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QY 422 GLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVVADAV 481  
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QY 447 GLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVVADAV 506  
Db |  
QY 482 KAQGA 487  
Db |  
QY 507 KAQGA 512

## RESULT 5

US-08-541-033A-2  
Sequence 2, Application US/08541033A  
Patent No. 5879941

```
/ GENERAL INFORMATION:
/ APPLICANT: Schmidt, Robert R.
/ APPLICANT: Miller, Philip
/ TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
/ TITLE OF INVENTION: RELATING TO THE A- AND -SUBUNITS OF GLUTAMATE
/ TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
/ NUMBER OF SEQUENCES: 26
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Saliwanchik & Saliwanchik
/ STREET: 2421 N.W. 41st Street, Suite A-1
/ CITY: Gainesville
/ STATE: Florida
/ COUNTRY: USA
/ ZIP: 32606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/541,033A
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Whitlock, Ted W.
/ REGISTRATION NUMBER: 36,965
/ REFERENCE/DOCKET NUMBER: UF155
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (904) 375-8100
/ TELEFAX: (904) 372-5800
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 526 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/
/ US-08-541-033A-2
/
/ Query Match 99.8%; Score 2508; DB 2; Length 526;
/ Best Local Similarity 100.0%; Pred. No. 1.3e-22;
/ Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 2 AVSLEQISAMDATTGDTALQKAVKQMATKAGTEGLVHGINKNPVDRQLLTETFMKDPQ 61
/ DB 41 AVSLEQISAMDATTGDTALQKAVKQMATKAGTEGLVHGINKNPVDRQLLTETFMKDPQ 100
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/ QY 62 QEFMQAVREVAVSLQVPFEKRPPELLPIFKQIPEPERVITFRVSWLDDAGNLQVNRGRVQ 121
/ DB 101 QEFMQAVREVAVSLQVPFEKRPPELLPIFKQIPEPERVITFRVSWLDDAGNLQVNRGRVQ 160
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/ QY 122 YSSAIGPYKGLRPHSPVNLNLSIMKFLAFQIFKNSLTTLPMGGGKGSDFDPKGSDAEV 181
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/ QY 182 MRFCOSFMTLQRHISYQVDPAGDIGVAREIGYLFQYKRITKNYTGVLTPKGOEYGG 241
/ DB 221 MRFCOSFMTLQRHISYQVDPAGDIGVAREIGYLFQYKRITKNYTGVLTPKGOEYGG 280
/
/ QY 242 SEIRPEATGYGAVLFVENVLKDKGSLKGRCLVSGAGNVAQYCAELLEKEGAILVLSLD 301
/ DB 281 SEIRPEATGYGAVLFVENVLKDKGSLKGRCLVSGAGNVAQYCAELLEKEGAILVLSLD 340
/
/ QY 302 SQGYVPEPNGFTREQQAQVDMKKKNSARISEYKSDTAVYVGDRRKPKWELDCQVDIAPP 361
/ DB 341 SQGYVPEPNGFTREQQAQVDMKKKNSARISEYKSDTAVYVGDRRKPKWELDCQVDIAPP 400
/
/ QY 362 CATQNEIDHDAELLIKHGCQYVVEGANPSTNEAIHKYNKAGIICYCKAANAGVAVS 421
/ DB 401 CATQNEIDHDAELLIKHGCQYVVEGANPSTNEAIHKYNKAGIICYCKAANAGVAVS 460
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/ QY 422 GLEMTQNRSLNWTREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAV 481
/ DB 461 GLEMTQNRSLNWTREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAV 520
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QY 482 KAQGA 487
DB 521 KAQGA 526

RESULT 6
US-08-828-451-2
/ Sequence 2, Application US/08828451
/ Patent No. 5985634
/ GENERAL INFORMATION:
/ APPLICANT: Schmidt, Robert R.
/ APPLICANT: Miller, Philip
/ TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
/ TITLE OF INVENTION: RELATING TO THE A- AND -SUBUNITS OF GLUTAMATE
/ TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
/ NUMBER OF SEQUENCES: 26
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Saliwanchik & Saliwanchik
/ STREET: 2421 N.W. 41st Street, Suite A-1
/ CITY: Gainesville
/ STATE: Florida
/ COUNTRY: USA
/ ZIP: 32606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/828,451
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/541,033
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Whitlock, Ted W.
/ REGISTRATION NUMBER: 36,965
/ REFERENCE/DOCKET NUMBER: UF155
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (904) 375-8100
/ TELEFAX: (904) 372-5800
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 526 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/
/ US-08-828-451-2
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Query Match 99.8%; Score 2508; DB 2; Length 526;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 2 AVSLEQISAMDATTGDTALQKAVKQMATKAGTEGLVHGINKNPVDRQLLTETFMKDPQ 61
/ DB 41 AVSLEQISAMDATTGDTALQKAVKQMATKAGTEGLVHGINKNPVDRQLLTETFMKDPQ 100
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/ QY 62 QEFMQAVREVAVSLQVPFEKRPPELLPIFKQIPEPERVITFRVSWLDDAGNLQVNRGRVQ 121
/ DB 101 QEFMQAVREVAVSLQVPFEKRPPELLPIFKQIPEPERVITFRVSWLDDAGNLQVNRGRVQ 160
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/ QY 122 YSSAIGPYKGLRPHSPVNLNLSIMKFLAFQIFKNSLTTLPMGGGKGSDFDPKGSDAEV 181
/ DB 161 YSSAIGPYKGLRPHSPVNLNLSIMKFLAFQIFKNSLTTLPMGGGKGSDFDPKGSDAEV 220
/
/ QY 182 MRFCOSFMTLQRHISYQVDPAGDIGVAREIGYLFQYKRITKNYTGVLTPKGOEYGG 241
/ DB 221 MRFCOSFMTLQRHISYQVDPAGDIGVAREIGYLFQYKRITKNYTGVLTPKGOEYGG 280
/
/ QY 242 SEIRPEATGYGAVLFVENVLKDKGSLKGRCLVSGAGNVAQYCAELLEKEGAILVLSLD 301
/ DB 281 SEIRPEATGYGAVLFVENVLKDKGSLKGRCLVSGAGNVAQYCAELLEKEGAILVLSLD 340
/
/ QY 302 SQGYVPEPNGFTREQQAQVDMKKKNSARISEYKSDTAVYVGDRRKPKWELDCQVDIAPP 361
/ DB 341 SQGYVPEPNGFTREQQAQVDMKKKNSARISEYKSDTAVYVGDRRKPKWELDCQVDIAPP 400
/
/ QY 362 CATQNEIDHDAELLIKHGCQYVVEGANPSTNEAIHKYNKAGIICYCKAANAGVAVS 421
/ DB 401 CATQNEIDHDAELLIKHGCQYVVEGANPSTNEAIHKYNKAGIICYCKAANAGVAVS 460
/
/ QY 422 GLEMTQNRSLNWTREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAV 481
/ DB 461 GLEMTQNRSLNWTREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAV 520
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Db 281 SEIRPEATGYGAVLFVENVLKKGESLKGKRCCLVSGAGNVAQYCAELLEKEGAIVLSLSD 340
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Db 341 SQGYVYEPNGFTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFP 400
Qy 362 CATONEIDEHDAELLKHGCOYVVEGANPSTNEAIHKYNKAGIIPCCKAANAGGVAVS 421
Db 401 CATONEIDEHDAELLKHGCOYVVEGANPSTNEAIHKYNKAGIIPCCKAANAGGVAVS 460
Qy 422 GLEMTQNRSLNWTREVRDRLERIMKDIYDSAMGPSRRYVNDVLAAGANITAGFTKVADAV 481
Db 461 GLEMTQNRSLNWTREVRDRLERIMKDIYDSAMGPSRRYVNDVLAAGANITAGFTKVADAV 520
Qy 482 KAQGA 487
Db 521 KAQGA 526

RESULT 7
US-08-541-033A-26
; Sequence 26, Application US/08541033A
; Patent No. 5879941
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,033A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UFI55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-541-033A-26

Query Match 98.1%; Score 2465; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.1e-218;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 MDATTGDFALQAVKQMATKAGTEGLVHGKINPDVRLTLTEIFMKDPQEQFMAQVREV 71
Db 1 MDATTGDFALQAVKQMATKAGTEGLVHGKINPDVRLTLTEIFMKDPQEQFMAQVREV 60
Qy 72 AVSLQPVFEKRELLPIFQIPEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 131
Db 61 AVSLQPVFEKRELLPIFQIPEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
```

```
Qy 132 GLRPHPSVNLSTMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFMT 191
Db 121 GLRPHPSVNLSTMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFMT 180
Qy 192 LQRHLSYQDVDPAGDIGVAREIGYLFQYKRTKNTYTGVLTPKGOEYGGSEIRPEATGY 251
Db 181 LQRHLSYQDVDPAGDIGVAREIGYLFQYKRTKNTYTGVLTPKGOEYGGSEIRPEATGY 240
Qy 252 GAVLFVENVLKDKGSLKGRCLVSGAGNVAQYCAELLEKEGAIVLSLSDSQGYVYEPNG 311
Db 241 GAVLFVENVLKDKGSLKGRCLVSGAGNVAQYCAELLEKEGAIVLSLSDSQGYVYEPNG 300
Qy 312 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPQATQNEIDEH 371
Db 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPQATQNEIDEH 360
Qy 372 DAELLIKHGCOYVVEGANPSTNEAIHKYNKAGIIPCCKAANAGGVAVSGLMTQNRMS 431
Db 361 DAELLIKHGCOYVVEGANPSTNEAIHKYNKAGIIPCCKAANAGGVAVSGLMTQNRMS 420
Qy 432 LNWTREVRDRLERIMKDIYDSAMGPSRRYVNDVLAAGANITAGFTKVADAVKAQGA 487
Db 421 LNWTREVRDRLERIMKDIYDSAMGPSRRYVNDVLAAGANITAGFTKVADAVKAQGA 476

RESULT 8
US-08-828-451-26
; Sequence 26, Application US/08828451
; Patent No. 5985634
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,451
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,033
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UFI55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-828-451-26

Query Match 98.1%; Score 2465; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.1e-218;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 12 MDATTGDTALQKAVQMATKAGTEGLVHGIKNPDVROLTLTEIFMKDPEQOEPMQAVREV 71  
DB 1 MDATTGDTALQKAVQMATKAGTEGLVHGIKNPDVROLTLTEIFMKDPEQOEPMQAVREV 60  
QY 72 AVSLQPVFEKRPPELLPIFKQIVPEPVIITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 131  
DB 61 AVSLQPVFEKRPPELLPIFKQIVPEPVIITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120  
QY 132 GLRPHSPVNLISIMKFLAFEQIFKNSLTTLPMGGGKGSDFDPKGSDAEVMRFQCSFMTE 191  
DB 121 GLRPHSPVNLISIMKFLAFEQIFKNSLTTLPMGGGKGSDFDPKGSDAEVMRFQCSFMTE 180  
QY 192 LQRHISVQVDPAGDIGVAREIGYLFQGYKRTIKNTYVGLTPKQGYGSEIRPEATGY 251  
DB 181 LQRHISVQVDPAGDIGVAREIGYLFQGYKRTIKNTYVGLTPKQGYGSEIRPEATGY 240  
QY 252 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLKGAIVLSLSDSQGYVYEPNG 311  
DB 241 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLKGAIVLSLSDSQGYVYEPNG 300  
QY 312 FTREQLQAVQDMKKONNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPFCATQNEIDEH 371  
DB 301 FTREQLQAVQDMKKONNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPFCATQNEIDEH 360  
QY 372 DAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIICPGKAANAGGVAVSGLEMTQNRMS 431  
DB 361 DAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIICPGKAANAGGVAVSGLEMTQNRMS 420  
QY 432 LNWTRREVRDKLERIMKDIYDSAMGPSRRNVNDLAAGANIAGTKVKADAVKAQAV 487  
DB 421 LNWTRREVRDKLERIMKDIYDSAMGPSRRNVNDLAAGANIAGTKVKADAVKAQAV 476

RESULT 9  
US-09-252-991A-20646  
; Sequence 20646, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 20646  
; LENGTH: 450  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-20646

Query Match 52.1%; Score 1309; DB 4; Length 450;  
Best Local Similarity 59.2%; Pred. No. 4.4e-112;  
Matches 263; Conservative 55; Mismatches 120; Indels 6; Gaps 4;

QY 47 VROLLTEIFMKDPEQOEPMQAVREAVSLQPVFEKRPPELLP--IFKQIVPEPVIITFRVS 104  
DB 10 VDAFLERLKRDDPDQEFHQAVEVLRSLWFFLEAPHYLEAGIIRIIVEPERAILFRVP 69  
QY 105 WLDDAGNLQVNRGFRVQYSSAIGPYKGLRPHSPVNLISIMKFLAFBQIFKNSLTTLPMGG 164  
DB 70 WVDQGRVVRNRYQVQMSAIGPYKGLRPHSPVNLGLVKLFLAFBQVFNKNSLTTLPMGG 129  
QY 165 KGGSDFDPKGSDAEVMRFQCSFMTELQRIHISVQVDPAGDIGVAREIGYLFQGYKRI 224  
DB 130 KGGSDFDPKGSDAEVMRFQCSFMTELRYHVGADLDVPAGDIGVAREIGYLFQGYKRI 189  
QY 225 TKNTYVGLTPKQGYGSEIRPEATGYGAVLFVENVLKDGESLKGKRCCLVSGAGNVAQY 284

DB 190 SNOFTSVLTGKLSYGSGLIRPEATGFCVYFAQEMLKDRGRGFCQORVAISSGNAQY 249  
QY 285 CAELLLKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKONNSARISEYKSDTAVYVG 344  
DB 250 AARKVMEMGGKVISLSDSEGTLYAEAGLSDQEWELMELKNVRR-GRIREMAEQFSLQFL 308  
QY 345 DRKPKWELDCQVDIAFPFCATQNEIDEHDAELLIKHGCOYVVEGANMPSTNEAIHKYNKAG 404  
DB 309 EGRRPWGLAC--DIALPCATQNEELDAEDARRLLANGCVCVAGGANMPSTLEAVDLFLEAG 366  
QY 405 IICPCPKAANAGGVAVSGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSA-MGPSRRYV 463  
DB 367 ILYAPKASNAGGVAVSGLEMSQNRMLRWSGEVDTKLHGIMQSIHHACLLYGESQGRV 426  
QY 464 DLAAGANIAGTKVKADAVKAQAV 487  
DB 427 NYVKGANIAGFVKVADAMLAQGVV 450

RESULT 10  
US-09-328-352-5725  
; Sequence 5725, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 5725  
; LENGTH: 467  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-5725

Query Match 50.0%; Score 1257.5; DB 4; Length 467;  
Best Local Similarity 55.9%; Pred. No. 2.6e-107;  
Matches 256; Conservative 61; Mismatches 128; Indels 13; Gaps 5;

QY 38 LVH-----GIKNPDVROLTLTEIFMKDPEQOEPMQAVREAVSLQPVFEKRPPELLP--IF 89  
DB 11 LIIHYAEDRALKYNLNEFLNYQARDPHQEPFLQAVEEVTSLWPFIEKNPEYAEQGLL 70  
QY 90 KQIVPEPVIITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGLRPHSPVNLISIMKFLAF 149  
DB 71 ERLVEPVIITFRVSWMDQGGQTQVNRAPRVQYNSAIGPFKGMRFHPSVNLISILKFLGF 130  
QY 150 BQIFKNSLTTLPMGGGKGSDFDPKGSDAEVMRFQCSFMTELQRIHISVQVDPAGDIGV 209  
DB 131 EOTFKNSLTTLPMGGGKGSDFPNPKGSDAEIMRFQCALMIELRYHLRGLPNTDIPAGDIGV 190  
QY 210 GARETGYPQYKRTIKNTYVGLTPKQGYGSEIRPEATGYGAVLFVENVLKDGESLK 269  
DB 191 GAREVGMAGMKKLSNDTACVFTGKGISFGSGLMRPEATGYGTVFAEEMLKTRKQSPA 250  
QY 270 GKRCCLVSGAGNVAQYCAELLLKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKONNS 329  
DB 251 GKTVSISSGSGNVAQYAAEKAMFLGAKVVTLSDSNGTVYLKNGFTDBELLAEMVLMKNIK- 309  
QY 330 ARISEYKSDTAVYVGDRRKPWELDCQVDIAFPFCATQNEIDEHDAELLIKHGCOYVVEGAN 389  
DB 310 GRISFASKHGFEPYEGKTPWHI--PVDIALPCATQNELTGEDAKTLTANGYICVAEGAN 367  
QY 390 MPSTNEAIHKYNKAGIICPGKAANAGGVAVSGLEMTQNRMSLNWTRREVRDKLERIMK 449  
DB 368 MPSTLEAVEBHFTEAKLILYAPKASNAGGVAVSGLEMSQNRMLRWSGEVDTKLHGIMQSIHHACLLYGESQGRV 427  
QY 450 IYDSAM--GPSRRYVNDLAAAGANIAGTKVKADAVKAQ 485  
DB 428 IHANCVRYGTBEDGTWNYVDGANIAGFVKVADAMLAQ 465





```

; FILING DATE: 01-JUL-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/021,058
; FILING DATE: 02-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kokulis, Paul K.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 81163/241766
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)-861-3503
; TELEFAX: (202)-822-0944
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 447 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; US-08-886-640-3

```

```

Query Match          47.8%; Score 1201; DB 2; Length 447;
Best Local Similarity 54.0%; Pred. No. 4e-102;
Matches 241; Conservative 67; Mismatches 128; Indels 10; Gaps 5;

```

```

QY 47 VRQLLTETFMKDPQEQBQPMQAVREAVSLQPVFEKRPDL--LPFKQIVPEPVRVITPRVS 104
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 7 LESFLNHVQKRDPNQTEPAQAVREVMTTLWPFLBQNPKYRQMSLLERLVEPVRVITPRV 66
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 105 WLDAGNLQVNRGFRVQVSSAIGPYKGLRPHSPVNLSTKFLAPEQIFKNSLTTLPMGG 164
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 67 WDDRNQIQVNRARVQFSSAIGPYKGMRFPHSPVNLSTLKLPLGPEQTFKNALTTLP 126
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 165 KGKGSDFDPKGSDAEVRFCQSPMTQLQRIHSYVDVPAGDIGVGAREIGYLFQYKRI 224
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 127 KGKGSDFDPKGSSEGVWRFQALMTLYRHLGADTDVPAGDIGVGAREIGYLFQYKRI 186
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 225 TKNTYGVLTTPKQYGGSEIRPEATGYGAVLFVENVLKDKGSLKGRKCLVSGAGNVAQY 284
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 187 SNNTACVFTKGLSFGGSLIRPEATGYGLVYFTTEAMLRKHGMFGEGMRVSVSGSNVAQY 246
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 285 CAELLEKGAVLSLSDSGYVVEPNFTREQLQAVQDMKKNSARISEYKSDTAVVVG 344
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 247 ALEKAMEFGARVITASDSSGTVVDESFTKEKLARLIEI-KASRDGRVADYAKFGLVYL 305
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 345 DRKPEWELDCQVDIAFPQCATQNEIDEHDAELLIKHGQYVVEGANMPSTNEAIHKYNKAG 404
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 306 EGQQPWSL--PVDIALPCATQNELDVAHQLIANGVKAEGANMPPTIEATELFPQAG 363
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 405 IYCFGKAANAGGAVSGLEMTQNRMSLNWTREVRDKLERIMKDIYDSAM---GPSRRY 461
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 364 VLFAPGKAANAGGAVATSGLEMAQNAARLGWKAERVDARLHMLDIIHACVDHGGEGEQT 423
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 462 NVDLAAGANIAGFTKVADAVKAQAV 487
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 424 N--YVQGANIAGFVKVADAMLAQGYI 447
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 14
US-08-884-235-11
; Sequence 11, Application US/08884235
; Patent No. 6329573
; GENERAL INFORMATION:
; APPLICANT: Lightfoot, David A.
; APPLICANT: Long, Lynn M.
; APPLICANT: Lightfoot, Maria E. Vidal
; TITLE OF INVENTION: PLANTS CONTAINING THE gsha GENE AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington

```

```

; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/884,235
; FILING DATE: 27-JUN-1997
; CLASSIFICATION: 800
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 447 residues
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; US-08-884-235-11

```

```

Query Match          47.8%; Score 1201; DB 3; Length 447;
Best Local Similarity 54.0%; Pred. No. 4e-102;
Matches 241; Conservative 67; Mismatches 128; Indels 10; Gaps 5;

```

```

QY 47 VRQLLTETFMKDPQEQBQPMQAVREAVSLQPVFEKRPDL--LPFKQIVPEPVRVITPRVS 104
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 7 LESFLNHVQKRDPNQTEPAQAVREVMTTLWPFLBQNPKYRQMSLLERLVEPVRVITPRV 66
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 105 WLDAGNLQVNRGFRVQVSSAIGPYKGLRPHSPVNLSTKFLAPEQIFKNSLTTLPMGG 164
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 67 WDDRNQIQVNRARVQFSSAIGPYKGMRFPHSPVNLSTLKLPLGPEQTFKNALTTLP 126
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 165 KGKGSDFDPKGSDAEVRFCQSPMTQLQRIHSYVDVPAGDIGVGAREIGYLFQYKRI 224
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 127 KGKGSDFDPKGSSEGVWRFQALMTLYRHLGADTDVPAGDIGVGAREIGYLFQYKRI 186
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 225 TKNTYGVLTTPKQYGGSEIRPEATGYGAVLFVENVLKDKGSLKGRKCLVSGAGNVAQY 284
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 187 SNNTACVFTKGLSFGGSLIRPEATGYGLVYFTTEAMLRKHGMFGEGMRVSVSGSNVAQY 246
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 285 CAELLEKGAVLSLSDSGYVVEPNFTREQLQAVQDMKKNSARISEYKSDTAVVVG 344
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 247 ALEKAMEFGARVITASDSSGTVVDESFTKEKLARLIEI-KASRDGRVADYAKFGLVYL 305
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 345 DRKPEWELDCQVDIAFPQCATQNEIDEHDAELLIKHGQYVVEGANMPSTNEAIHKYNKAG 404
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 306 EGQQPWSL--PVDIALPCATQNELDVAHQLIANGVKAEGANMPPTIEATELFPQAG 363
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 405 IYCFGKAANAGGAVSGLEMTQNRMSLNWTREVRDKLERIMKDIYDSAM---GPSRRY 461
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 364 VLFAPGKAANAGGAVATSGLEMAQNAARLGWKAERVDARLHMLDIIHACVDHGGEGEQT 423
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 462 NVDLAAGANIAGFTKVADAVKAQAV 487
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 424 N--YVQGANIAGFVKVADAMLAQGYI 447
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 15
US-08-370-193A-11
; Sequence 11, Application US/08370193A
; Patent No. 5573945
; GENERAL INFORMATION:
; APPLICANT: ONO, EIJI
; APPLICANT: TSUJIMOTO, NORIHARU
; APPLICANT: MATSUI, KAZUHIKO
; APPLICANT: KURAHASHI, KAZUHIKO
; TITLE OF INVENTION: MUTANT AND METHOD FOR PRODUCING
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; P.C.

```



STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
 CITY: ARLINGTON  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/370,193A  
 FILING DATE: 09-JAN-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OBLON, NORMAN F.  
 REGISTRATION NUMBER: 24,618  
 REFERENCE/DOCKET NUMBER: 10-714-0  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-413-3000  
 TELEFAX: 703-413-2220  
 TELEX: 248855 OPAT UR  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 447 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-370-193A-11

Query Match 47.8%; Score 1200; DB 1; Length 447;  
 Best Local Similarity 54.0%; Pred. No. 4.9e-102;  
 Matches 241; Conservative 67; Mismatches 128; Indels 10; Gaps 5;

|    |     |  |     |
|----|-----|--|-----|
| QY | 47  | VRQLLTETFMKDEQEEFMQAVREAVSLQPVFEKPEL--LPFKQIVPEPERVITERVS    | 104 |
| Db | 7   | LESFLNHVQKDPNQTEFAQAQREVTTLWFLFQNKPKYRQMSLLERLVEPERVIOFRVV   | 66  |
| QY | 105 | WLDDAGNLQVRGFRVQYSSAIGPYKGLRFPHSVNLISIMKFLAFEQIFKNSLITLPMGG  | 164 |
| Db | 67  | WYDRNQIQVNRARVQFSASIGPYKGNRFPHSVNLISILKFLGFEQTFKNALITLPMGG   | 126 |
| QY | 165 | HGKGSDFDPKGSADAVRMFCQSFMTTELORHISYVDVPAGDIGVGAREIGYLFQYKRI   | 224 |
| Db | 127 | HGKGSDFDPKGSSEGVNRFQALMTLYRHLGADTDVPAGDIGVGREGVFMAGWMKKL     | 186 |
| QY | 225 | TKNYTCVLTLPKQEGYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKCLVSGAGNVAQY | 284 |
| Db | 187 | SNNTACVFTGKGLSFGSLIRPEATGYGLVYFTEAMLKRHGMGFEGMRVSVSGGNVAQY   | 246 |
| QY | 285 | CAELLLEKGAIVLSLSDSQGYVVEPNQFTREOLQAVODMKKNNNSARISEYKSDTAVYVG | 344 |
| Db | 247 | ALEKAMEFGARVITASDSSGTVDSESGFTKEKLRLIEI-KASRDGRVADYAKERGLVYL  | 305 |
| QY | 345 | DRKPMELDCQVDIAPPQATQNEIDHDAELIKHGCGYVVEGANNPSTNEAIHKYNKAG    | 404 |
| Db | 306 | EGQPWLSL--PVDIALPCATQNELDVAHAQLIANGKAVAEAGANNPTTIEATLFFQQAG  | 363 |
| QY | 405 | IYCPCKAANAGGAVSGLEMTQNRMSLNWTRVEEVDKLERIMKDIYDSAM--GPSRRY    | 461 |
| Db | 364 | VLPAPGAANAGGVATSGLEMPQNAARLGMKAEKVDAARLHHIMLDITHHACVHGGEQET  | 423 |
| QY | 462 | NYDLAAGANIAGFTKVADAVKAGAV                                    | 487 |
| Db | 424 | N--YVQGANIAGFVKVADAMLQGV                                     | 447 |

Search completed: September 8, 2005, 02:12:07  
 Job time : 27.0834 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 8, 2005, 02:12:18 ; Search time 88.1553 Seconds  
(without alignments)  
2828.902 Million cell updates/sec

Title: US-10-627-886-24

Perfect score: 2513

Sequence: 1 MAVSLEEISAMDAITGDTT.....GANIAGFTKVADAVKQAGAV 487

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID        | Description        |
|------------|--------|-------------|--------|--------------|--------------------|
| 1          | 2446   | 97.3        | 523    | 1 DHE4_CHLSO | P28998 chlorella s |
| 2          | 1375   | 54.7        | 510    | 2 Q81LF7     | Q81lf7 plasmodium  |
| 3          | 1361   | 54.2        | 1203   | 2 Q7RQ39     | Q7rq39 plasmodium  |
| 4          | 1328   | 52.8        | 446    | 2 Q7VZU9     | Q7vzu9 spironucleu |
| 5          | 1327.5 | 52.8        | 449    | 2 Q7R3N7     | Q7r3n7 giardia lam |
| 6          | 1324.5 | 52.7        | 449    | 1 DHE4_GIALA | P28724 giardia lam |
| 7          | 1309   | 52.1        | 445    | 2 Q9HVJ7     | Q9hvj7 pseudomonas |
| 8          | 1300.5 | 51.8        | 444    | 2 Q9JY71     | Q9jy71 neisseria m |
| 9          | 1294.5 | 51.5        | 444    | 2 Q9JT56     | Q9jt56 neisseria m |
| 10         | 1287.5 | 51.2        | 449    | 2 Q8RQ23     | Q8rq23 pseudomonas |
| 11         | 1286.5 | 51.2        | 470    | 2 Q8E940     | Q8e940 plasmodium  |
| 12         | 1286.5 | 51.2        | 470    | 2 Q8ILU0     | Q8ilt0 plasmodium  |
| 13         | 1285   | 51.1        | 445    | 2 Q9Z3C4     | Q9z3c4 pseudomonas |
| 14         | 1284.5 | 51.1        | 437    | 2 Q7VZU7     | Q7vzu7 trichomonas |
| 15         | 1265   | 50.3        | 442    | 2 Q9TXS8     | Q9txs8 plasmodium  |
| 16         | 1264   | 50.3        | 442    | 2 Q9TKS5     | Q9tk5 plasmodium   |
| 17         | 1257   | 50.0        | 465    | 2 Q6S143     | Q6s143 uncultured  |
| 18         | 1253.5 | 49.9        | 536    | 2 Q7RG75     | Q7rgt5 plasmodium  |
| 19         | 1250.5 | 49.8        | 448    | 2 Q8G6L0     | Q8g6l0 bifidobacte |
| 20         | 1250.5 | 49.8        | 455    | 2 Q8G872     | Q8g872 ruminococcu |
| 21         | 1249.5 | 49.7        | 447    | 2 Q6FD67     | Q6fd67 acinetobact |
| 22         | 1241.5 | 49.4        | 448    | 2 Q8XK85     | Q8xk85 clostridium |
| 23         | 1240.5 | 49.4        | 449    | 2 Q8E4J6     | Q8e4j6 streptococc |
| 24         | 1239.5 | 49.3        | 448    | 2 Q835G2     | Q835g2 enterococcu |
| 25         | 1238   | 49.3        | 449    | 1 DHE4_HAEIN | P43793 haemophilus |
| 26         | 1236.5 | 49.2        | 449    | 2 Q8DY77     | Q8dy77 streptococc |
| 27         | 1234   | 49.1        | 447    | 2 Q61083     | Q61083 trypanosoma |
| 28         | 1231.5 | 49.0        | 462    | 2 Q65W57     | Q65w57 manheimia   |
| 29         | 1230.5 | 49.0        | 449    | 2 Q8DUL2     | Q8dul2 streptococc |
| 30         | 1230   | 48.9        | 449    | 2 Q9CPJ4     | Q9cpj4 pasteurella |
| 31         | 1225.5 | 48.8        | 444    | 1 DHE3_BACTN | P94598 bacteroides |

|    |        |      |     |              |                    |
|----|--------|------|-----|--------------|--------------------|
| 32 | 1225   | 48.7 | 448 | 2 Q9AIW1     | Q9aiw1 streptococc |
| 33 | 1214.5 | 48.3 | 444 | 1 DHE4_PRERU | P95544 prevotella  |
| 34 | 1214   | 48.3 | 448 | 2 Q8DPG0     | Q8dpg0 streptococc |
| 35 | 1212   | 48.2 | 448 | 2 Q97QB4     | Q97qb4 streptococc |
| 36 | 1210.5 | 48.2 | 458 | 2 Q9KB34     | Q9kb34 bacillus ha |
| 37 | 1206.5 | 48.0 | 447 | 2 Q7VSN6     | Q7vsn6 bordetella  |
| 38 | 1205.5 | 48.0 | 424 | 2 Q9NTN9     | Q9ntn9 deinococcus |
| 39 | 1205.5 | 48.0 | 444 | 2 Q64Q81     | Q64q81 bacteroides |
| 40 | 1205.5 | 48.0 | 464 | 2 Q7WEU7     | Q7weu7 bordetella  |
| 41 | 1202   | 47.8 | 448 | 2 Q88XM9     | Q88xm9 lactobacill |
| 42 | 1201   | 47.8 | 447 | 1 DHE4_ECOLI | P00370 escherichia |
| 43 | 1200.5 | 47.8 | 446 | 2 Q60956     | Q60956 trypanosoma |
| 44 | 1200   | 47.8 | 449 | 2 Q6AJB1     | Q6ajb1 desulfotale |
| 45 | 1199   | 47.7 | 443 | 2 Q97L29     | Q97l29 clostridium |

ALIGNMENTS

|          |  |           |      |         |  |
|----------|--|-----------|------|---------|--|
| RESULT 1 |  |           |      |         |  |
| ID       | DHE4_CHLSO   | STANDARD; | PRT; | 523 AA. |  |
| AC       | P28998;  |           |      |         |  |
| DT       | 01-DEC-1992 (Rel. 24, Created)   |           |      |         |  |
| DT       | 01-DEC-1992 (Rel. 24, Last sequence update)                                |           |      |         |  |
| DT       | 29-MAR-2004 (Rel. 43, Last annotation update)                              |           |      |         |  |
| DE       | NADP-specific glutamate dehydrogenase (EC 1.4.1.4) (NADP-GDH)              |           |      |         |  |
| DE       | (Fragment)   |           |      |         |  |
| OS       | Chlorella sorokiniana.   |           |      |         |  |
| OC       | Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;     |           |      |         |  |
| OC       | Chlorellaceae; Chlorella.  |           |      |         |  |
| OX       | NCBI TaxID=3076;   |           |      |         |  |
| RN       | [1]  |           |      |         |  |
| RP       | SEQUENCE FROM N.A.   |           |      |         |  |
| RX       | MEDLINE=92032762; PubMed=1718478;  |           |      |         |  |
| RA       | Cock J.M., Kim K.D., Miller P.W., Hutson R.G., Schmidt R.R.;               |           |      |         |  |
| RT       | "A nuclear gene with many introns encoding ammonium-inducible              |           |      |         |  |
| RT       | chloroplastic NADP-specific glutamate dehydrogenase(s) in Chlorella        |           |      |         |  |
| RT       | sorokiniana."  |           |      |         |  |
| RL       | Plant Mol. Biol. 17:1023-1044(1991).                                       |           |      |         |  |
| CC       | -!- CATALYTIC ACTIVITY: L-glutamate + H(2)O + NADP(+) = 2-oxoglutarate     |           |      |         |  |
| CC       | + NH(3) + NADPH.   |           |      |         |  |
| CC       | -!- SUBUNIT: Homo- and heterohexamer of alpha and beta subunits. Both      |           |      |         |  |
| CC       | subunits are encoded by the same gene.                                     |           |      |         |  |
| CC       | -!- SUBCELLULAR LOCATION: Chloroplast.                                     |           |      |         |  |
| CC       | -!- INDUCTION: By ammonium   |           |      |         |  |
| CC       | -!- PTM: The N-termini of the alpha and the beta chains are blocked.       |           |      |         |  |
| CC       | -!- SIMILARITY: Belongs to the Glu/Leu/Phe/Val dehydrogenases family.      |           |      |         |  |
| CC       | -----  |           |      |         |  |
| CC       | This SWISS-PROT entry is copyright. It is produced through a collaboration |           |      |         |  |
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| CC       | entities requires a license agreement (See http://www.isb-sib.ch/announce/ |           |      |         |  |
| CC       | or send an email to license@isb-sib.ch).                                   |           |      |         |  |
| CC       | -----  |           |      |         |  |
| DR       | EMBL; X58832; CAA41636.1; -  |           |      |         |  |
| DR       | EMBL; X58831; CAA41635.1; ALT_SEQ.   |           |      |         |  |
| DR       | PIR; S17949; S17949.   |           |      |         |  |
| DR       | HSP; P24295; LAUP.   |           |      |         |  |
| DR       | InterPro; IPR006095; GLFV_dehydrog.  |           |      |         |  |
| DR       | InterPro; IPR006096; GLFV_dehydrog_C.                                      |           |      |         |  |
| DR       | InterPro; IPR006097; GLFV_dehydrog_N.                                      |           |      |         |  |
| DR       | Pfam; PF0208; GLFV_dehydrog; 1.  |           |      |         |  |
| DR       | Pfam; PF02812; GLFV_dehydrog_N; 1.   |           |      |         |  |
| DR       | PRINTS; PR00082; GLFDHGNASE.   |           |      |         |  |
| DR       | PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.                                   |           |      |         |  |
| DR       | Chloroplast; NADP; Oxidoreductase.   |           |      |         |  |
| KW       | NON_TER 1  |           |      |         |  |
| FT       | ACT_SITE 202 202   |           |      |         |  |
| FT       | SEQUENCE 523 AA; 57529 MW; A35FE730B5FEF974 CRC64;                         |           |      |         |  |
| FT       | By similarity.   |           |      |         |  |



RL Nature 419:512-519 (2002).  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL: AABL01000331, EAA20557.1, --.  
DR HSSP: P24295; 1AUP.  
DR GO: GO:0016491; F:oxidoreductase activity; IEA.  
DR GO: GO:0006520; P:amino acid metabolism; IEA.  
DR InterPro: IPR005135; Exo\_endo\_phos.  
DR InterPro: IPR006095; GLFV dehydrog.  
DR InterPro: IPR006096; GLFV dehydrog\_C.  
DR InterPro: IPR006097; GLFV dehydrog\_N.  
DR Pfam: PF03372; Exo\_endo\_phos; 1.  
DR Pfam: PF0208; GLFV dehydrog; 1.  
DR Pfam: PF02812; GLFV dehydrog\_N; 1.  
DR PRINTS: PR00082; GLFV dehydrog\_N; 1.  
DR PROSITE: PS00074; GLFV dehydrog\_N; 1.  
SQ SEQUENCE 1203 AA; 13909 MW; DBE1988BD4C21715 CRC64;

Query Match 54.2%; Score 1361; DB 2; Length 1203;  
Best Local Similarity 59.3%; Pred. No. 1.9e-85;  
Matches 264; Conservative 65; Mismatches 108; Indels 8; Gaps 5;

QY 47 VRQLLTETIFMKDPEQEFMQAVREAVSLQPVFEKRPPELLPIFKQIVPEPVIITFRVSWL 106  
Db 763 IEMKENVISKNKQDHEFLQAFEEVLTSLKPVFKNIYYLGVLENISEPVIQPRVPMI 822  
QY 107 DDAGNLQVNRGFRVQYSSAIGPYKGLRFPSPNSIMKFLAFEPQIFKNSLTTLPMGGGK 166  
Db 823 NDNGEHKINRGFRVQYSSVILGPKYKGLRFPSPNSIMKFLAFEPQIFKNSLTTLPMGGGK 882  
QY 167 GGSDFDPKGSDAEVMRFQCSFMTELQRIHSYVDVPAGDIGVAREIGYLFQGYKRIITK 226  
Db 883 GGSDFDPKGSSENEILRFQCSFMDNLFVYIGPNTDIPAGDIGVAREIGYLFQGYKRIITK 942  
QY 227 NTGVLTTPKQGYGSEIRPEATGYGAVLFVENVLKDGESLKGKRCVSGAGNAQYCA 286  
Db 943 KFEGLVTGKNIKGGSGNIRSEATGYGAVFAENALSDMNEKNTKTCVSGGNAQYLV 1002  
QY 287 ELLLEKGAIVLSLSDSQYVYVPENGFTREQLQAVQDMKKNSARISEY--KSDTAVYVG 344  
Db 1003 ELLLEKGAIVLSLSDSQYVYVPENGFTREQLQAVQDMKKNSARISEY--KSDTAVYVG 344  
QY 345 DRKKPWLQCDVDIAPPCATQNEIDHDAELIKHGCGQYVVEGANMPSNEAIHKYNKAG 404  
Db 1061 ENKPNVFC--DIVPFCATQNEITENDADLIKNCKLLVSGANMPTHIKAWHLKENK 1118  
QY 405 ILYCPGKAANAGGAVVSGLEMTQNRMSLNTWREVRDKLERIMKDIYDSAMGFSRRY--N 462  
Db 1119 ILICPSKAANAGGAVVSGLEMTQNRMSLNTWREVRDKLERIMKDIYDSAMGFSRRY--N 462  
QY 463 VDLAAGANTAGFTKADAVKAQAV 487  
Db 1179 TDLVAGANTAGFTKADSVFIEQGL 1203

RESULT 4  
QY7ZU9 ID Q7Y2U9 PRELIMINARY; PRT; 446 AA.  
AC Q7Y2U9  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 26, Last annotation update)  
DE Glutamate dehydrogenase (Fragment).  
OS Name=gdh;  
GN Spiroonucleus barthansu.  
OC Eukaryota; Diplomonadida; Hexamitidae; Hexamitinae; Spiroonucleus.  
OX NCBI\_TaxID=103874;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 50380;  
RX PubMed=12820901; DOI=10.1186/1471-2148-3-14;  
RA Andersson J.O., Roger A.J.;

RT "Evolution of glutamate dehydrogenase genes: evidence for lateral gene  
RT transfer within and between prokaryotes and eukaryotes.";  
RL BMC Evol. Biol. 3:14-14 (2003).  
DR EMBL: AF533884; MAP83851.1; --.  
DR HSSP: P24295; 1AUP.  
DR GO: GO:0016491; F:oxidoreductase activity; IEA.  
DR GO: GO:0006520; P:amino acid metabolism; IEA.  
DR InterPro: IPR006095; GLFV dehydrog.  
DR InterPro: IPR006096; GLFV dehydrog\_C.  
DR InterPro: IPR006097; GLFV dehydrog\_N.  
DR Pfam: PF0208; GLFV dehydrog; 1.  
DR Pfam: PF02812; GLFV dehydrog\_N; 1.  
DR PROSITE: PS00074; GLFV dehydrog\_N; 1.  
SQ SEQUENCE 446 AA; 49309 MW; AEB43D2A1762DB80 CRC64;

Query Match 52.8%; Score 1328; DB 2; Length 446;  
Best Local Similarity 58.6%; Pred. No. 1e-83;  
Matches 262; Conservative 65; Mismatches 110; Indels 10; Gaps 6;

QY 46 DVROLLTETIFMKDPEQEFMQAVREAVSLQPVFEKRPPELLPIFKQIVPEPVIITFRVSW 105  
Db 5 DKNVLTQ---RDANIEFCQAVNEIDSLTVFEENPKYISVFQQLLEPERVIMFRVPM 61  
QY 106 LDDAGNLQVNRGFRVQYSSAIGPYKGLRFPSPNSIMKFLAFEPQIFKNSLTTLPMGGG 165  
Db 62 TDDKGEVINRGYRVQYNSALGPYKGLRFPSPNSIMKFLAFEPQIFKNSLTTLPMGGG 121  
QY 166 KGSDFDPKGSDAEVMRFQCSFMTELQRIHSYVDVPAGDIGVAREIGYLFQGYKRIIT 225  
Db 122 KGSDFDPKGSNGEVMRFQCSFMTELQRIHSYVDVPAGDIGVAREIGYLFQGYKRIIT 181  
QY 226 KNYTGLTTPKQGYGSEIRPEATGYGAVLFVENVLKDGESLKGKRCVSGAGNAQYCA 285  
Db 182 NOFTGILTKGAYSWGSGSLRPEATGYGAVYVYVPENGFTREQLQAVQDMKKNSARISEY-- 241  
QY 286 AELLLEKGAIVLSLSDSQYVYVPENGFTREQLQAVQDMKKNSARISEY--KSDTAVYV 343  
Db 242 TEKLLHYGAIPLSLSDSNGTIEPFGPTAEQLKXWMDLKNYK-GRLESEYTSMSSTAKY 300  
QY 344 GDRKPWL-DCQVDIAPPCATQNEIDHDAELIKHGCGQYVVEGANMPSNEAIHKYNK 402  
Db 301 -EGQRPWAVYEGVDVIMPCATQNEVNGTEAERVIKGLRVYVSEGANMPSNDDAIHAYS 359  
QY 403 AGIYCPSKAANAGGAVVSGLEMTQNRMSLNTWREVRDKLERIMKDIYDSAMGFSRRY 462  
Db 360 SKVYFGPAKAGGAVVSGLEMTQNRMSLNTWREVRDKLERIMKDIYDSAMGFSRRY 419  
QY 463 V--DLAAGANTAGFTKADAVKAQAV 487  
Db 420 KKGNYQFGANVAGFLKADSMIDQCV 446

RESULT 5  
QY7R3N7 ID Q7R3N7 PRELIMINARY; PRT; 449 AA.  
AC Q7R3N7  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE GLP 39 39379 38030.  
OS Giardia lamblia ATCC 50803.  
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.  
OX NCBI\_TaxID=184922;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WB C6;  
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,  
RA Olsen G.J., Sogin M.L.;  
RT "Draft sequence of the Giardia lamblia genome.";  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

```

CC preliminary data.
DR EMBL; AACB01000014; EAA1919.1; -.
DR HSSP; P24295; LAUP.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV dehydrog.
DR InterPro; IPR006096; GLFV dehydrog. C.
DR InterPro; IPR006097; GLFV dehydrog. N.
DR Pfam; PF02008; GLFV dehydrog. 1.
DR PRINTS; PR00082; GLFDHGRNASE.
DR PROSITE; PS00074; GLFV DEHYDROGENASE; 1.
SQ SEQUENCE 449 AA; 49734 MW; 2397B34FBEBCEAE2 CRC64;

Query Match 52.8%; Score 1327.5; DB 2; Length 449;
Best Local Similarity 58.4%; Pred. No. 1.1e-83;
Matches 261; Conservative 66; Mismatches 111; Indels 9; Gaps 5;

QY 47 VRLQLTEIFMKDPEQOEPMQAVREAVVLSQVPEKRPPELLPIFKQIVPERVITFRVSWL 106
DB 6 ISELAVIKQDGHMTFRQAVVEVDLSKVIFEREPKYIPERMLSPERVIIFRVPWM 65

QY 107 DDAGNLQVNRGRFVQYSSAIGPYKGLRPHSPVNSLIMKFLAFQIFKNSLTLLPMGGGK 166
DB 66 DDAGRLNVNRGRFVQYNSALGPYKGLRPHSPVNSLILKFLGFQELKNSLTLLPMGGGK 125

QY 167 GGSDFDPKGSDAEVMRFQSQFMTLQRIHSYVDVPAGDIGVAREIGYLPFGQYKRITK 226
DB 126 GGSDFDPKGSDAEVMRFQSQFMTLQRIHSYVDVPAGDIGVAREIGYLPFGQYKRITK 185

QY 227 NYTGVLTTPKQGEYGGSEIRPEATGYGAVLFVENVLKDGESLKGKRCILVSGAGNVAQYCA 286
DB 186 EFTGVLTGKNVKGWGSFIRPEATGYGAVYFLEEMCKDNNTVIRGKNVLLSGSNVAQYCA 245

QY 287 ELLLEKGAIVLSLSDSQYVYEPNGFTREQLQAVQDMKKKNSARISEYKS---DTAVV 343
DB 246 EKLILQAKVLTFSDSNGTIYDKGFNEEKLALHMYLKNKR-GRVSEFKDYPVAYYE 304

QY 344 GDRRPWE-LDCQVDIAPFCATONEIDEHDAELLIKHGQYVVEGANPNSTNEAIHKYNK 402
DB 305 G--KKPWECEFGQMDICMPATQNEVSGDDATRLVGLGLKFAVGANPNSTAEAVHYHA 362

QY 403 AGIICYPCGAANAGGAVVSGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGSRRYN 462
DB 363 KGMVYGPAPKASNAGGVSGLSEMSQNSVRLQWTAEBVDQKLGRIMRGIFVACRDTAKKYG 422

QY 463 --VDLAAGANIAGFTKVADAVKAQAV 487
DB 423 HPKNYQMGANIAGFLKVADSMIEQGCY 449

RESULT 6
ID DHE4_GIALA STANDARD; PRT; 449 AA.
AC P28724; Q24961;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 29-MAR-2004 (Rel. 43, Last annotation update)
DE NADP-specific glutamate dehydrogenase (EC 1.4.1.4) (NADP-GDH) (NADP-dependent glutamate dehydrogenase).
OS Giardia lamblia (Giardia intestinalis).
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=5741;
RN MEDLINE=92218410; PubMed=1559991;
RA Yee J., Dennis P.P.;
RT isolation and characterization of a NADP-dependent glutamate dehydrogenase gene from the primitive eucaryote Giardia lamblia.;
RL J. Biol. Chem. 267:7539-7544(1992).
RN (2)
RP SEQUENCE OF 59-261 FROM N.A.
RX MEDLINE=96155200; PubMed=8587793;

```

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RA Monis P.T., Mayrhofer G., Andrews R.H., Homan W.L., Limper L.,
RA By P.L.;
RT "Molecular genetic analysis of Giardia intestinalis isolates at the
RT glutamate dehydrogenase locus.";
RL Parasitology 112:1-12(1996).
CC -!- CATALYTIC ACTIVITY: L-glutamate + H(2)O + NADP(+) = 2-oxoglutarate
CC + NH(3) + NADPH.
CC -!- SUBUNIT: Homohexamer (By similarity).
CC -!- SIMILARITY: Belongs to the Glu/Leu/Phe/Val dehydrogenases family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M84604; AAA29155.1; -.
CC EMBL; U47632; AAB05400.1; -.
CC PIR; A42489; A42489.
CC HSSP; P24295; LAUP.
CC InterPro; IPR006095; GLFV dehydrog.
CC InterPro; IPR006096; GLFV dehydrog. C.
CC InterPro; IPR006097; GLFV dehydrog. N.
CC Pfam; PF02008; GLFV dehydrog. 1.
CC PRINTS; PR00082; GLFDHGRNASE.
CC PROSITE; PS00074; GLFV DEHYDROGENASE; 1.
KW NADP: Oxidoreductase.
FT ACT_SITE 125 125 By similarity.
FT CONFLICT 249 249 I -> L (in Ref. 2).
FT SEQUENCE 449 AA; 49766 MW; 5497B35209B549F6 CRC64;

Query Match 52.7%; Score 1324.5; DB 1; Length 449;
Best Local Similarity 58.2%; Pred. No. 1.8e-83;
Matches 260; Conservative 67; Mismatches 111; Indels 9; Gaps 5;

QY 47 VRLQLTEIFMKDPEQOEPMQAVREAVVLSQVPEKRPPELLPIFKQIVPERVITFRVSWL 106
DB 6 ISELAVIKQDGHMTFRQAVVEVDLSKVIFEREPKYIPERMLSPERVIIFRVPWM 65

QY 107 DDAGNLQVNRGRFVQYSSAIGPYKGLRPHSPVNSLIMKFLAFQIFKNSLTLLPMGGGK 166
DB 66 DDAGRLNVNRGRFVQYNSALGPYKGLRPHSPVNSLILKFLGFQELKNSLTLLPMGGGK 125

QY 167 GGSDFDPKGSDAEVMRFQSQFMTLQRIHSYVDVPAGDIGVAREIGYLPFGQYKRITK 226
DB 126 GGSDFDPKGSDAEVMRFQSQFMTLQRIHSYVDVPAGDIGVAREIGYLPFGQYKRITK 185

QY 227 NYTGVLTTPKQGEYGGSEIRPEATGYGAVLFVENVLKDGESLKGKRCILVSGAGNVAQYCA 286
DB 186 EFTGVLTGKNVKGWGSFIRPEATGYGAVYFLEEMCKDNNTVIRGKNVLLSGSNVAQYCA 245

QY 287 ELLLEKGAIVLSLSDSQYVYEPNGFTREQLQAVQDMKKKNSARISEYKS---DTAVV 343
DB 246 EKLILQAKVLTFSDSNGTIYDKGFNEEKLALHMYLKNKR-GRVSEFKDYPVAYYE 304

QY 344 GDRRPWE-LDCQVDIAPFCATONEIDEHDAELLIKHGQYVVEGANPNSTNEAIHKYNK 402
DB 305 G--KKPWECEFGQMDICMPATQNEVSGDDATRLVGLGLKFAVGANPNSTAEAVHYHA 362

QY 403 AGIICYPCGAANAGGAVVSGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGSRRYN 462
DB 363 KGMVYGPAPKASNAGGVSGLSEMSQNSVRLQWTAEBVDQKLGRIMRGIFVACRDTAKKYG 422

QY 463 --VDLAAGANIAGFTKVADAVKAQAV 487
DB 423 HPKNYQMGANIAGFLKVADSMIEQGCY 449

RESULT 7
Q9HJ7

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ID Q9HJV7 PRELIMINARY; PRT; 445 AA.
AC Q9HJV7;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Glutamate dehydrogenase.
GN Name-gdhA; OrderedLocusNames=PA4588;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; AE004872; AAC07976.1; -.
DR PIR; H83072; H83072.
DR HSP; P24295; 1AUP.
DR GO; GO:0016491; P:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV dehydrog.
DR InterPro; IPR006096; GLFV dehydrog_C.
DR InterPro; IPR006097; GLFV dehydrog_N.
DR Pfam; PF0208; GLFV dehydrog_1.
DR Pfam; PF02812; GLFV dehydrog_N; 1.
DR PRINTS; PR00082; GLFDHGRNASE.
DR PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
KW Complete proteome.
SQ SEQUENCE 445 AA; 48856 MW; 643EB12BC84F3418 CRC64;

Query Match 52.1%; Score 1309; DB 2; Length 445;
Best Local Similarity 59.2%; Pred. No. 2.1e-82;
Matches 263; Conservative 55; Mismatches 120; Indels 6; Gaps 4;

QY 47 VRLQLTEIFMKDPEQOEQMAVREAVSLQPVFEKRPPELLP--IPKQIVEPERVITFRVS 104
Db 5 VDAFLERLKRDPDQPEPHQAVEEVLRLSLWPLEANPHYLEAGIIRIVERPERAILFRVP 64

QY 105 WLDDAGNLQVNRGFRVQYSSAIGPYKGLRPHSPVNLIMKFLAFEPQFNKSLTTLPMG 164
Db 65 WYDDQGRVNRGFRVQYSSAIGPYKGLRPHSPVNLIMKFLAFEPQFNKSLTTLPMG 124

QY 165 GKGGSDFPDPKGSDAEVMRFQSFMTLQRIHSYVDVPAGDVGAREIGYLFQYKRI 224
Db 125 GKGGSDFPDPKGSDAEVMRFQSFMTLQRIHSYVDVPAGDVGAREIGYLFQYKRI 184

QY 225 TKNYTVGLTPKQYGGSSIRPEATGYGAVLFVENVLKDKGSLKGRCLVSGAGNVAQY 284
Db 185 SNQFTSVLTGKGLSGSLIRPEATGYGAVLFVENVLKDKGSLKGRCLVSGAGNVAQY 244

QY 285 CAELLEKGAIVLSLSDSGYVYENGFTREQLQAVQDMKKKNNSARISEYKSDTAVYG 344
Db 245 AARKVMEMGKVIISLSDSEGLTYAAGLSDEQWELMELKNVR--GRITREMAEQSLQFL 303

QY 345 DRKPKWELDCQVDIAPPCATONEIDEHDAELLIKHCQVYVEGANPSTNEAIHKYNKAG 404
Db 304 BGRFPWGLAC--DIALPCATQNELDABARRLLANGCVCVAGGANPSTLEAVDLFLFAG 361

QY 405 IYCPGKAAGAGVAVSGLEMTQNRMSLNWTREVRDKLERIMKDIYDSA-MGPRRRYNY 463
Db 362 ILIYAFKASAGVAVSGLEMSQNRMLRWSSEGVDTKLHGIMQSIHACLLYGEQGRV 421

QY 464 DIAAGANTAGFTKVADAVKQAGV 487

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Db 422 NYVKGANIAGFVKVADAMLAQGVV 445

RESULT 8
Q9JY71 PRELIMINARY; PRT; 444 AA.
AC Q9JY71;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Glutamate dehydrogenase, NADP-specific.
GN OrderedLocusNames=NMB1710;
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
RA Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
RA Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,
RA Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,
RA Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,
RA Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H.M.,
RA Qin H., Vamathevan J.J., Gill J., Scarlato V., Maignani V., Pizza M.,
RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
RA Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58.";
RL Science 287:1809-1815(2000).
DR EMBL; AE002521; AAF42057.1; -.
DR PIR; H81050; H81050.
DR HSP; P24295; 1AUP.
DR TIGR; NMB1710; -.
DR GO; GO:0016491; P:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV dehydrog.
DR InterPro; IPR006096; GLFV dehydrog_C.
DR InterPro; IPR006097; GLFV dehydrog_N.
DR Pfam; PF0208; GLFV dehydrog_1.
DR Pfam; PF02812; GLFV dehydrog_N; 1.
DR PRINTS; PR00082; GLFDHGRNASE.
DR PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
KW Complete proteome.
SQ SEQUENCE 444 AA; 48490 MW; 8B2CFCCA89EF7DAF CRC64;

Query Match 51.8%; Score 1300.5; DB 2; Length 444;
Best Local Similarity 57.4%; Pred. No. 8.2e-82;
Matches 257; Conservative 72; Mismatches 104; Indels 15; Gaps 6;

QY 46 DVRLQLTEIFMKDPEQOEQMAVREAVSLQPVFEKRPPELLP--PIFKQIVEPERVITFRV 103
Db 3 DLNTLFANLKNRPNQEPFHQAVEEVLRLSLWPLEANPHYLEAGIIRIVERPERVIMFRV 62

QY 104 SWLDDAGNLQVNRGFRVQYSSAIGPYKGLRPHSPVNLIMKFLAFEPQFNKSLTTLPMG 163
Db 63 TWQDDKGVQVNRGFRVQYSSAIGPYKGLRPHSPVNLIMKFLAFEPQFNKSLTTLPMG 122

QY 164 GKGGSDFPDPKGSDAEVMRFQSFMTLQRIHSYVDVPAGDVGAREIGYLFQYKRI 223
Db 123 GKGGSDFPDPKGSDAEVMRFQSFMTLQRIHSYVDVPAGDVGAREIGYLFQYKRI 182

QY 224 ITKNYTVGLTPKQYGGSSIRPEATGYGAVLFVENVLKDKGSLKGRCLVSGAGNVAQ 283
Db 183 IRNBFSSVLTGKGLSGSLIRPEATGYGAVLFVENVLKDKGSLKGRCLVSGAGNVAQ 242

QY 284 YCAELLEKGAIVLSLSDSGYVYENGFTREQLQAVQDMKKKNNSARISEYKSDTAVY 342
Db 243 YAAEKALQIGAKVLTVSDSNGFVLFPDPSGMTQAALALIELKEVRRE-RVATYAKEQGLQ 301

QY 343 VGDRRKWELDCQVDIAPPCATONEIDEHDAELLIKHCQVYVEGANPSTNEAIHKYNK 402

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QY 165 GKGSDPDPKGSDDAEVWRFQSGFWTELRQHRHSYYVDVPAGDIGVGARIGYLFQGYKRI 224
DB 128 GKGSDPDPKGSDDAEVWRFQSGFWTELRQHRHSYYVDVPAGDIGVGARIGYLFQGYKRI 187
QY 225 TKNYTGVLTPKGOEYCGSIRPEATGYGAVLFVENVLKDKGSLKGRCLVSGAGNVAQY 284
DB 188 ANOFTSVLTKGMYGGSIRPEATGYGAVLFVENVLKDKGSLKGRCLVSGAGNVAQY 247
QY 285 CAELLEKGAIVLSDSDSQYVYPNGFTREQLQAVQDMKKKNNSARISEYKSDTAVVYG 344
DB 248 AARKVMDLGGKVISLSDSEGTLVYAEAGLTDAQWDLALMELKNVYK-GRISELAGQFCLEPR 306
QY 345 DRKPWELQCDVDIAPPQATONEIDHDAELLKHGCGQYVVEGANMPSNTEAHKYNKAG 404
DB 307 KGOTWPSLPC--DIALPQATONELGAEDARTLLRNGCICVAGANNPTTLEAVDIFLDAG 364
QY 405 IYCPGKAANAGVAVSGLEMTQNRMSLNWTRREYVDKLERIMKDIYDSAM--GPSRRYN 462
DB 365 ILYAPKASNAGVAVSGLEMTQNRMSLNWTRREYVDKLERIMKDIYDSAM--GPSRRYN 424
QY 463 VDLAAGANIAGFTKVADAVKAQAV 487
DB 425 INVKGANIAGFTKVADAVKAQAV 449

RESULT 11
O96940 PRELIMINARY; PRT; 470 AA.
AC O96940;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Glutamate dehydrogenase (NADP+) (EC 1.4.1.4).
GN Name=GludH; Synonymes=GDH;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99089647; PubMed=9874251;
RA Wagner J.T., Juedemann H., Faerber P.M., Lottspeich F.,
RA Krauth-Siegel R.L.;
RT "Glutamate dehydrogenase, the marker protein of Plasmodium falciparum.
RT Cloning, expression and characterization of the malarial enzyme.";
RL Eur. J. Biochem. 258:813-819(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Li L.H., Li M., Wu Y.S., Wang P.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y12927; CAA73390.1; -.
DR EMBL; AY040586; AAK77969.1; -.
DR HSSP; P24295; 1AUP.
DR GO; GO:0004354; F:glutamate dehydrogenase (NADP+) activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV dehydrog.
DR InterPro; IPR006095; GLFV dehydrog.
DR InterPro; IPR006097; GLFV dehydrog_N.
DR Pfam; PF0208; GLFV dehydrog; 1.
DR Pfam; PF02812; GLFV dehydrog N; 1.
DR PRINTS; PR00082; GLFDHNRGNASE.
DR PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
KW Oxidoreductase.
SQ SEQUENCE 470 AA; 52546 MW; 50A37C23484C387A CRC64;

Query Match 51.2%; Score 1286.5; DB 2; Length 470;
Best Local Similarity 55.2%; Pred. No. 8.3e-81;
Matches 266; Conservative 64; Mismatches 133; Indels 19; Gaps 7;

QY 9 ISAMDATGDTALQAVKQMATKAGTEGLVHGKIPNDVROLTLTEIFMKDPEQQEFMQAV 68
DB 1 MSALDKDKTRGFVLDK-----NASNYESLV-----DQEMNNVYERVMKLDPNQVBFLOAF 50

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QY 69 REVAVSLQVFEKRPPELLPIPKQIYVEPVRVITFRVSWLDDAGNLQVNRGFRVQYSATGP 128
DB 51 HEILYSLKPLFMWBBPKYLPITETLSEPERAIQIFVCMWDDNGVQRKNCRFRVQYNSALGP 110
QY 129 YKGLRFPSPVNLSTMKFLAPBQIFKNSLTITLPMCGGKGSGSDFDPKGSKSDAEWRFQCSF 188
DB 111 YKGLRFPSPVNLSTMKFLAPBQIFKNSLTITLPMCGGKGSGSDFDPKGSKSDAEWRFQCSF 170
QY 189 MTELQRHSYYVDVPAGDIGVGARIGYLFQGYKRIITKNYTGVLTPKGOEYCGSIRPEA 248
DB 171 MNELYRHGIPCTDVPAGDIGVGARIGYLFQGYKRIITKNYTGVLTPKGOEYCGSIRPEA 230
QY 249 TGYGAVLFVENVLKDKGSLKGRCLVSGAGNVAQYCAELLEKGAIVLSDSDSQYVYE 308
DB 231 TGYGLVYFVLEVLKSLNIPVEKQTAVVSGSGNVALYCVQKLHLNVKVLTLSDSNGYVYE 290
QY 309 PNGFTREQLQAVQDMKKKNNSARISEY--KSDTAVVYVGGRRKRWELDCQVDIAFCATON 366
DB 291 PNGFTREQLQAVQDMKKKNNSARISEY--KSDTAVVYVGGRRKRWELDCQVDIAFCATON 346
QY 367 EIDEHDAELLKHGCGQYVVEGANMPSNTEAHKYNKAGIYCPGKAANAGVAVSGLEMT 426
DB 347 EINLEDKLLQKNGCILVEGANMPSNTEAHKYNKAGIYCPGKAANAGVAVSGLEMT 406
QY 427 QNRMSLNWTRREYVDKLERIMKDIYDSAMGPSRRY---NVDLAAGANIAGFTKVADAVKA 483
DB 407 QNFQPSHWTRVDEKLEIMENFIACSENALKYTKNKYDLQACANIAGFLKVAESYE 466
QY 484 QG 485
DB 467 QG 468

RESULT 12
Q8ILTO PRELIMINARY; PRT; 470 AA.
AC Q8ILTO;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE NADP-specific glutamate dehydrogenase.
GN ORFNames=PF14_0164;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
RA Gardiner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum."
RL Nature 419:498-511(2002).
DR EMBL; AE014818; AAN36776.1; -.
DR HSSP; P24295; 1AUP.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV dehydrog.
DR InterPro; IPR006096; GLFV dehydrog C.
DR InterPro; IPR006097; GLFV dehydrog_N.
DR Pfam; PF0208; GLFV dehydrog; 1.
DR Pfam; PF02812; GLFV dehydrog N; 1.
DR PRINTS; PR00082; GLFDHNRGNASE.
DR PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
SQ SEQUENCE 470 AA; 52546 MW; 50A37C23484C387A CRC64;

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Search completed: September 8, 2005, 02:43:30  
Job time : 90.1553 secs

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| Result No. | Query  |       |        | DB | ID     | Description        |
|------------|--------|-------|--------|----|--------|--------------------|
|            | Score  | Match | Length |    |        |                    |
| 1          | 2446   | 97.3  | 523    | 1  | S17949 | glutamate dehydrog |
| 2          | 1324.5 | 52.7  | 449    | 1  | A42489 | glutamate dehydrog |
| 3          | 1309   | 52.1  | 445    | 2  | H83072 | glutamate dehydrog |
| 4          | 1300.5 | 51.8  | 444    | 2  | H81050 | glutamate dehydrog |
| 5          | 1294.5 | 51.5  | 444    | 2  | B81825 | glutamate dehydrog |
| 6          | 1238   | 49.3  | 449    | 2  | A64053 | glutamate dehydrog |
| 7          | 1214.5 | 48.3  | 444    | 2  | T10487 | glutamate dehydrog |
| 8          | 1214   | 48.3  | 448    | 2  | D98019 | glutamate dehydrog |
| 9          | 1212   | 48.2  | 448    | 2  | H95151 | NADP-specific glut |
| 10         | 1210.5 | 48.2  | 458    | 2  | E83912 | NADP-specific glut |
| 11         | 1205.5 | 48.0  | 424    | 2  | E75362 | glutamate dehydrog |
| 12         | 1201   | 47.8  | 447    | 1  | DESCEN | glutamate dehydrog |
| 13         | 1199   | 47.7  | 443    | 2  | F96990 | NADP-specific glut |
| 14         | 1198   | 47.7  | 447    | 2  | C90937 | NADP-specific glut |
| 15         | 1198   | 47.7  | 447    | 2  | G85785 | NADP-specific glut |
| 16         | 1189.5 | 47.3  | 458    | 2  | A11503 | NADP-specific glut |
| 17         | 1185   | 47.2  | 447    | 2  | S32227 | glutamate dehydrog |
| 18         | 1182   | 47.0  | 447    | 1  | A33504 | glutamate dehydrog |
| 19         | 1181   | 47.0  | 447    | 2  | AF0710 | NADP-specific glut |
| 20         | 1180.5 | 47.0  | 458    | 2  | A11144 | NADP-specific glut |
| 21         | 1153   | 45.9  | 447    | 2  | AE0483 | glutamate dehydrog |
| 22         | 1150   | 45.8  | 448    | 2  | D64567 | glutamate dehydrog |
| 23         | 1143   | 45.5  | 450    | 2  | S23403 | glutamate dehydrog |
| 24         | 1142.5 | 45.5  | 448    | 2  | B95277 | probable glutamate |
| 25         | 1139   | 45.3  | 448    | 2  | F71862 | glutamate dehydrog |
| 26         | 1133.5 | 45.1  | 446    | 2  | S06938 | glutamate dehydrog |
| 27         | 1121.5 | 44.6  | 454    | 1  | DENCEN | glutamate dehydrog |
| 28         | 1115.5 | 44.4  | 459    | 1  | S49904 | glutamate dehydrog |
| 29         | 1109   | 44.1  | 457    | 2  | S63608 | glutamate dehydrog |

QY 242 SEIRPEATGYGAVLFVENVLKDGBSLKGRCLVSGAGNVAQYCAELLLKGAIVLSLD 301  
Db 278 SEIRPEATGYGAVLFVENVLKDGBSLKGRCLVSGAGNVAQYCAELLLKGAIVLSLD 337  
QY 302 SQGYVYEPNGFTREQLQAVQDMKKNNNSARISEYKSDTAVYVGGDRRKPEWELDCQVDIAPP 361  
Db 338 SQGYVYEPNGFTREQLQAVQDMKKNNNSARISEYKSDTAVYVGGDRRKPEWELDCQVDIAPP 397  
QY 362 CATONEIDEHDAELLIKHGCGQVYVGGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVS 421  
Db 398 CATONEIDEHDAELLIKHGCGQVYVGGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVS 457  
QY 422 GLEMTQNRMSLNMTREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAV 481  
Db 458 GLEMTQNRMSLNMTREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAV 517  
QY 482 KAQGAV 487  
Db 518 KAQGAV 523  
RESULT 2  
A:Accession: A42489  
Glutamate dehydrogenase (NADP) [EC 1.4.1.4] - Giardia lamblia  
N:Alternate names: glutamic dehydrogenase; NADP-specific glutamate dehydrogenase  
C:Species: Giardia lamblia  
C:Date: 31-Dec-1993 #sequence\_revision 23-Mar-1995 #text\_change 09-Jul-2004  
A:Accession: A42489  
R:Yee, J.; Dennis, P.P.  
J. Biol. Chem. 267, 7539-7544, 1992  
A:Title: Isolation and characterization of a NADP-dependent glutamate dehydrogenase gene  
A:Reference number: A42489; MUID:92218410; PMID:1559991  
A:Accession: A42489  
A:Molecule type: DNA  
A:Residues: 1-449 <YEE>  
A:Cross-references: UNIPROT:P28724; GB:M84604; NID:g159108; PIDN:AAA29155.1; PID:g159109  
A:Note: sequence extracted from NCBI backbone (NCBI:94071, NCBI:P94074)  
C:Superfamily: glutamate dehydrogenase (NAD(P)+)  
C:Keywords: NADP; oxidoreductase  
F:125/Binding site: substrate (Lys) #status predicted  
Query Match 52.7%; Score 1324.5; DB 1; Length 449;  
Best Local Similarity 58.2%; Pred. No. 1.9e-90;  
Matches 260; Conservative 67; Mismatches 111; Indels 9; Gaps 5;  
QY 47 VRQLLTFIMKDPQEQBFMAQVREAVAVSLQPVFEKRPPELLPTFKQIVPEPVIITFRVSWL 106  
Db 6 IBEELAVIKQRDGHMTEFRAQVEEVVDSLSKVIFEREPKYIPIFERMLPEPVIITFRVPMW 65  
QY 107 DDAGNLQVNRGRVQYSSAIGPYKGLRPHSPVNLSIMKFLAFEQIFKNSLTTLPMGGGK 166  
Db 66 DDAGNLQVNRGRVQYSSAIGPYKGLRPHSPVNLSIMKFLAFEQIFKNSLTTLPMGGGK 125  
QY 167 GGSDFDPKGSDAEVMRFQSPMTLORHISVQVDPAGDIGVAREIGYLFQGYKRLN 226  
Db 126 GGSDFDPKGSDAEVMRFQSPMTLORHISVQVDPAGDIGVAREIGYLFQGYKRLN 185  
QY 227 NYTGVLTTPKGQBYGSGEIRPEATGYGAVLFVENVLKDGBSLKGRCLVSGAGNVAQYCA 286  
Db 186 EFTGVLTGKNVKGSGFIRPEATGYGAVYFLBEMCKDNTVIRGNVLLSGSNVAQFAC 245  
QY 287 ELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKNNNSARISEYKS---DTAVYV 343  
Db 246 EKLIQLGAKVLTFSDSNGTIVDKDGFNEBKLAHLMLYLNKRA-GRVSFVKDYPSPVAYYE 304  
QY 344 GDRRPWE-LDCQVDIAFPCCATONEIDEHDAELLIKHGCGQVYVGGANMPSTNEAIHKYNK 402  
Db 305 G--KKPWEFCFEGQMCIMPATQNEVSGDDATRLVGLGLKFVAEGANMPSTNEAIHKYNK 362  
QY 403 AGIYCPGKAANAGGVAVSGLGEMTQNRMSLNMTREVRDKLERIMKDIYDSAMGPSRRYN 462  
Db 363 KGVMTGPAKASNAGGVAVSGLGEMTQNRMSLNMTREVRDKLERIMKDIYDSAMGPSRRYN 422

QY 463 --VDLAAGANITAGFTKVADAVKAQAV 487  
Db 423 HPKQYQMGANTAGFLKVADSMIEQGCV 449  
RESULT 3  
H83072  
glutamate dehydrogenase PA4588 [imported] - Pseudomonas aeruginosa (strain PAO1)  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
A:Accession: H83072  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho  
gen  
A:Reference number: A82950; MUID:20437337; PMID:10984043  
A:Accession: H83072  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-445 <STO>  
A:Cross-references: UNIPROT:Q9HVJ7; GB:AE004872; GB:AE004091; NID:g9950829; PIDM:AAG0797  
A:Experimental source: strain PAO1  
C:Genetics:  
A:Gene: gdhA, PA4588  
C:Superfamily: glutamate dehydrogenase (NAD(P)+)  
Query Match 52.1%; Score 1309; DB 2; Length 445;  
Best Local Similarity 59.2%; Pred. No. 2.6e-89;  
Matches 263; Conservative 55; Mismatches 120; Indels 6; Gaps 4;  
QY 47 VRQLLTFIMKDPQEQBFMAQVREAVAVSLQPVFEKRPPELLP--IFKQIVPEPVIITFRVS 104  
Db 5 VDAFLERLKRDPQPEPHQAVEVLRSLWPFLEANPHYLEAGIIRIVEPERAILFRVP 64  
QY 105 WLDDAGNLQVNRGRVQYSSAIGPYKGLRPHSPVNLSIMKFLAFEQIFKNSLTTLPMGG 164  
Db 65 WDDQGRVVRNRYGVQVQSSAIGPYKGLRPHSPVNLGLVFLAFEPQVFKNSLTTLPMGG 124  
QY 165 KGGSDPDPKGSDAEVMRFQSPMTLORHISVQVDPAGDIGVAREIGYLFQGYKRI 224  
Db 125 KGGSDPDPKGSDAEVMRFQSPMTLORHISVQVDPAGDIGVAREIGYLFQGYKRL 184  
QY 225 TKNYTVLTTPKGQBYGSGEIRPEATGYGAVLFVENVLKDGBSLKGRCLVSGAGNVAQY 284  
Db 185 SNQFTSVLTGKLSYGGSLIRPEATGFCGYFAQEBMLKDRGFGDQGVVAISGSGNVAQY 244  
QY 285 CAELLLKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKNNNSARISEYKSDTAVYV 344  
Db 245 AARKVMEGKGKVISLSDSSEGLTYAEAGLSDEQWYLMELKNVRR-GRIREMAEQFSLOPL 303  
QY 345 DRRPWE-LDCQVDIAFPCCATONEIDEHDAELLIKHGCGQVYVGGANMPSTNEAIHKYNKAG 404  
Db 304 EGRPWEGLAC--DIALPCATONELDAEDARLLANGCVCVAEGANMPSTLEAVDLFLEAG 361  
QY 405 IYICPGKAANAGGVAVSGLGEMTQNRMSLNMTREVRDKLERIMKDIYDSA-MGPSRRYV 463  
Db 362 ILYAPGRKASNAGGVAVSGLGEMTQNRMSLNMTREVRDKLERIMKDIYDSA-MGPSRRYV 421  
QY 464 DLAAGANITAGFTKVADAVKAQAV 487  
Db 422 NYVKGANTAGPVKVADAMLAQGVV 445  
RESULT 4  
H81050  
glutamate dehydrogenase, NADP-specific NMB1710 [imported] - Neisseria meningitidis (stra  
in)  
C:Species: Neisseria meningitidis  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
A:Accession: H81050  
R:Tetzelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Bisen, J.A.;  
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;



|   |                       |   |                    |            |             |
|---|-----------------------|---|--------------------|------------|-------------|
|   | Query Match           | 51.5%   | Score 1294.5;      | DB 2;      | Length 444; |
|   | Best Local Similarity | 57.1%;  | Pred. No. 3.le-88; |            |             |
|   | Matches 256;          | Conservative 72;  | Mismatches 105;    | Indels 15; | Gaps 6      |
| / | 46                    | DVRQLLTETFMKDPQEQEFMQAEVAVSLQPVTEKRPELL--PFFKOIVPEPERVITPRV               | 103                |            |             |
| / |                       | :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   : |                    |            |             |
| D | 3                     | DLNTLFAVLKORNPQNPFHQAEVEVFMSLDPFLAKNPKYTQQSLLERIVEPERVVMPRV               | 62                 |            |             |
| / | 104                   | SWLDDAGNLQVNRGRFVQYSSAIGPYKGGLRPHSPVNLISMKFLAFEPQIFKNLSLTLPWG             | 163                |            |             |
| D | 63                    | TWQDDKGQVQVNRGRYVRQMSSAIGPYKGGLRFHPFTVDLVGILKFLAFEQVFNKALTLPWG            | 122                |            |             |
| / | 164                   | GKKGGSDPDPKGSNDARVMVRFCQGEMTPIQRHISVQDVDRAGDTCVGAPRTCYLRCQVDR             | 223                |            |             |

[illegible]

**Accession:** A64053  
**Status:** nucleic acid sequence not shown; translation not shown  
**Molecule type:** DNA  
**Residues:** 1-449 <**TIGR**>  
**Cross-references:** UNIPROT:P43793; GB:U32704; GB:L42023; NID:g1573143; PIDN:AAR  
**Superfamily:** glutamate dehydrogenase (**NAD(P)+**)  
**Keywords:** NADP; oxidoreductase

|      |   |  |
|------|---|--|
|      | Query Match   | 49.3%; Score 1238; DB 2; Length 449;   |
|      | Best Local Similarity   | 55.6%; Pred.No 5e-84;                  |
|      | Matches 247; Conservative   | 64; Mismatches 117; Indels 16; Gaps 5; |
| <br> | <div style="font-family: monospace; font-size: small;">           51 LTEIFMDKPEQEFMQAVREYVVSLOVFKEKRPELL--PIFKVIIEPERVVITFRVSLDD 108<br/>                ::                                                           :<br/>           11 LTAKAQRDGPFLQAAREFVFSINWPLEANPKYSEALLERLVFERAFQVRATDD 70<br/>                ::                                                                  </div> |  |
| <br> | <div style="font-family: monospace; font-size: small;">           109 AGNLQNRRGPRVQYSIGAIPKYGLGRPHPSVNLSIMKFLAPEIQFNKSLLTLPMSGKGKG 168<br/>                .:                                                                             </div>  |  |
| <br> | <div style="font-family: monospace; font-size: small;">           71 KGQOVNVNRPVQPNNSAIGPFKGMGRFHSPSNLISKPLGFQEIQFNALTTLPMGGAAGGG 130<br/>                .:                                                                             </div>   |  |
| <br> | <div style="font-family: monospace; font-size: small;">           169 SDPPDKGSDAENVNRFCQSFTWLQLRHHSYYVDVPAGDIGVGAREIIVLFQGYCRKITKNY 228<br/>                .:                                                                             </div>   |  |

Db 131 SDFDPKGSDAEVMRFQALMAELVYRHVGDVDPAGDVGVRGVLGYAGYMKKLSNQS 190  
Qy 229 TGVLTPKQGEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKCLVSGAGNVAQYCAEL 288  
Db 191 ACVFTGRGLSFGSLIRPEATGYGLTYFAQAMLAESKGSFAGKVVSVSGSGNVAQYAIK 250  
Qy 289 LLEKGAIVLSLSDSGYVYEPNGFTREQLQAVODMKKKNNSARISEYKSDTAVVYVDRRK 348  
Db 251 ALSGAKVVTCSDSGIVYDPNGFTTEKLAALFDI-KNTRGRVXDYAEQFGLQYFEGKR 309  
Qy 349 PHELDQVDIAFPQCATQNEIDHDAELLIKHGCVVVEGANMPSTNEAIHKYNKAGIYIC 408  
Db 310 PHEV--QVDIALPCATQNELESDAQLIKNGVKLVAEGANWPTTIEATEALLAADVLEF 367  
Qy 409 PKAANAGGAVVSGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRY----- 461  
Db 368 PKAANAGGAVATSGLEMAQSSORLYWTAEBVDQALHRLMLDIHANC---KKYGTIEGQE 423  
Qy 462 NYDLAAGANIAGTKVADAVKAQG 485  
Db 424 NINYVVGANVAVFKVADAWLAQG 447

## RESULT 7

T10487

glutamate dehydrogenase (NADP) (EC 1.4.1.4) - Prevotella ruminicola

C:Species: Prevotella ruminicola

C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004

C:Accession: T10487

R:Wen, Z.T.; Morrison, M.

submitted to the EMBL Data Library, December 1996

A:Reference number: Z17049

A:Accession: T10487

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-444 &lt;WEN&gt;

A:Cross-references: UNIPROT:P95544; EMBL:U82240; NID:g1772844; PID:g1772845

A:Experimental source: strain B14

C:Genetics:

A:Note: gdhA

C:Superfamily: glutamate dehydrogenase (NAD(P)+)

C:Keywords: NADP; oxidoreductase

Query Match 48.3%; Score 1214.5; DB 2; Length 444;  
Best Local Similarity 54.9%; Pred. No. 2.7e-82;  
Matches 242; Conservative 73; Mismatches 119; Indels 7; Gaps 4;

Qy 49 QLLTEIFMKDPEQEFMQAVREVAVLSQVPEKRPDL--LPFKQIVPEPVTITRVSNL 106  
Db 5 EVIEKKAKFPQGEYTIQAVSVQLGTIEEYKNHPEFEKANLIERLCVDPRIQLQFRVSV 64  
Qy 107 DDAGNLQVNRGRFVQYSSAIGPYKGLRPHSPVNLISIMKFLAFEQIFKNSLTLLPMGGGK 166  
Db 65 DNGNVQTNLGRVQHNAIGPYKGLRPHKSVNASILKFLAFEQIFKNSLTLLPMGGAK 124  
Qy 167 GGSDFDPKGSDAEVMRFQCSFMTELORHISVQDVPAGDIGVAREIGYLFQGYKRTK 226  
Db 125 GGSDFDPKGSDEVMRFQCSFMTELRLIGPDEDVPAGDIGVGRGVGMFGQYKKLTH 184  
Qy 227 NTGTVLTPKQGEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKCLVSGAGNVAQYCA 286  
Db 185 QFGILTGKLEFGGSLIRPEATGYGNVYFLEDMLKTRGESLEGKTVLVSSGSGNVAQYTI 244  
Qy 287 ELLEKGAIVLSLSDSGYVYEPNGFTREQLQAVODMKKKNNSARISEYKSDTAVVYVDR 346  
Db 245 EKLQLGAKPVCSDSNGIYDPDGIDAELKLAFLAFIMELKNVKR-GRKEYAEKVGKYVEN 303  
Qy 347 RKPWELDCQVDIAFPQCATQNEIDHDAELLIKHGCVVVEGANMPSTNEAIHKYNKAGTI 406  
Db 304 ARPW--GEKADIATPCATQDEINEAEAKTLIANGVFAVSEGANMPTEPAAIKVFQDAKIL 361  
Qy 407 YCPGKAANAGGAVVSGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAM--GPSRRYND 464

Db 362 YCPKASNAGGAVATSGLEMSQNSERLSWTRREVDTKLHNIMDEIHCNVCYKGTBPDGYIN 421  
Qy 465 LAAGANIAGTKVADAVKAQG 485  
Db 422 YVKGANVAGFMKAVAKAMMAQG 442  
RESULT 8  
D98019  
glutamate dehydrogenase (NADP) (EC 1.4.1.4) [imported] - Streptococcus pneumoniae (strain  
C:Species: Streptococcus pneumoniae  
C:Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 09-Jul-2004  
C:Accession: D98019  
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E  
y, P.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M  
J. Bacteriol. 183, 5709-5717, 2001  
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaaskunas, S.R.;  
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
A:Reference number: A97872; MUID:21429245; PMID:11544234  
A:Accession: D98019  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-448 <KUR>  
A:Cross-references: UNIPROT:Q8DPG0; GB:AE007317; PIDN:AAK99984.1; PID:g15458813; GSPDB:B  
C:Genetics:  
A:Gene: gdhA  
C:Superfamily: glutamate dehydrogenase (NAD(P)+)  
C:Keywords: oxidoreductase

Query Match 48.3%; Score 1214; DB 2; Length 448;  
Best Local Similarity 55.7%; Pred. No. 3e-82;  
Matches 248; Conservative 62; Mismatches 127; Indels 8; Gaps 4;  
Qy 47 VRQLLTEIFMKDPEQEFMQAVREVAVLSQVPEKRPDL--LPFKQIVPEPVTITRVSV 104  
Db 8 IQSFVETVKARNGHEAEFLQAVEFFNLEPVFEKHPYIEENTLARTETERVISFRVP 67  
Qy 105 WLDDAGNLQVNRGRFVQYSSAIGPYKGLRPHSPVNLISIMKFLAFEQIFKNSLTLLPMGG 164  
Db 68 WVDKRGKQVNRGRVQVNSAVGPYKGLRPHPTVNOGILKFLGPEQIFKXNLTGLPIGG 127  
Qy 165 GKSDFDPKGSDAEVMRFQCSFMTELORHISVQDVPAGDIGVAREIGYLFQGYKRI 224  
Db 128 GKSDFDPKGTDAEVMRFQCSFMTELQKHGSPSLDPAGDIGVGRGREGIYLYQYKRL 187  
Qy 225 TKNTVGLTPKQGEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKCLVSGAGNVAQY 284  
Db 188 NQPDAGVLTKPLGFGGSLIRPEATGYGLVYTYTEMLKANGSPAGKVKVIVSGSGNVAQY 247  
Qy 285 CAELLEKGAIVLSLSDSGYVYEPNGFTREQLQAVODMKKKNNSARISEYKSDTAVVYG 344  
Db 248 ALQKATELGATVISVSDSNGYVIDENGI---DFDLVDVKEKRR-ARLTYAAEKATATY 303  
Qy 345 DRRKPWELDCQVDIAFPQCATQNEIDHDAELLIKHGCVVVEGANMPSTNEAIHKYNKAG 404  
Db 304 HEGSVTYTAGNYDIALPCATQNEINGEAARLQAGVICVSEGANMPNLDIAIKYKENG 363  
Qy 405 IYCPGKAANAGGAVVSGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRYNV- 463  
Db 364 IFYGPAAKAGGAVVSALEMSQNSLRLSWTRREVDGRLKDIMNIFNTAKTTSETYGLD 423  
Qy 464 -DLAAGANIAGTKVADAVKAQGAV 487  
Db 424 KDYLAGANIAAFENVANAMIAQIV 448

## RESULT 9

H95151

NADP-specific glutamate dehydrogenase [imported] - Streptococcus pneumoniae (strain TIGR

C:Species: Streptococcus pneumoniae

C:Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 09-Jul-2004

C:Accession: H95151



QY 183 RFCSFMTLORHISVYQVDPAGDIGVGAREIGYLFGQVKRITKNYTGVLTPKGQYCGS 242  
Db 121 RFQALMTLWRLHGLDPTDVPAGDIGVGRREVGYLAGMMKLANHAGGVFTGKGLSYGGS 180  
QY 243 EIRPEATGYGAVLFVENVLKDGESLKGKRCIVSGAGNVAQYCAELLLEKGAIVLSLSDS 302  
Db 181 LLRPEATGYGVYFVEHMLRDQRMEMEGLRVSVSGSGNVAQYAIKALHGLHVLTSNS 240  
QY 303 QGYVPEPNTFREQLOAVQVDMKKKNSARISYKSDTAVYVQDRKRPWELDCQVDIAPPC 362  
Db 241 GGTVVDDEGFTYDKLAVLMDIKNERR-GRVEDYAREVGAEPFPGVRPW--DVPVDVALPC 297  
QY 363 ATQNEIDEHDAELLKHGCOYVVEGANMPSTNEATHYKNKAGIICYPCGKAANAGGVAVSG 422  
Db 298 ATQNSBLGADDARTLTAGGVVRVVAEGANMPCDLAAIOAPEEAGVLVAPGKATNAGGAVTSG 357  
QY 423 LEMTQNRSLNWTREVRDKLRIMKDIYDSAMGPSRR--YNVDLAAGANTAGFTKVVADA 480  
Db 358 LEMSQAQLSWTRREVDQRLRSIMSAHDSCLLEYGRPPDRHVSYLDQANTAGFVKVATA 417  
QY 481 VKAQGAV 487  
Db 418 MREQGV 424

RESULT 12  
DSECEN  
N:Alternate names: glutamate dehydrogenase; NADP-specific glutamate dehydrogenase  
C:Species: Escherichia coli  
C>Date: 03-Aug-1984 #sequence revision 20-Sep-1984 #text\_change 09-Jul-2004  
C:Accession: A00382; A22413; A64936  
R:McPherson, M.J.; Wootton, J.C.  
Nucleic Acids Res. 11, 5257-5266, 1983  
A:Title: Complete nucleotide sequence of the Escherichia coli gdhA gene.  
A:Reference number: A00382; MUID:83272967; PMID:6308576  
A:Accession: A00382  
A:Title: Complete nucleotide sequence of the glutamate dehydrogenase gene from Escherichia coli.  
A:Reference number: A22413; MUID:84209849; PMID:6373501  
A:Accession: A22413  
A:Molecule type: DNA  
A:Residues: 1-447 <MCP>  
A:Cross-references: UNIPROT:P00370; GB:X00988; GB:J01615; GB:X00565; NID:g41543; PIDN:CA  
R:Valle, F.; Becerril, B.; Chen, E.; Seeburg, P.; Heyneker, H.; Bolivar, F.  
Gene 27, 193-199, 1984  
A:Title: Complete nucleotide sequence of the glutamate dehydrogenase gene from Escherichia coli.  
A:Reference number: A22413; MUID:84209849; PMID:6373501  
A:Accession: A22413  
A:Molecule type: DNA  
A:Residues: 1-447 <VAL>  
A:Experimental source: strain K12  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co  
A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617; PMID:9278503  
A:Accession: A64936  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-447 <BLAT>  
A:Cross-references: GB:AE000271; GB:U00096; NID:g1788058; PIDN:AAC74831.1; PID:g1788059;  
A:Experimental source: strain K-12, substrain MG1655  
C:Genetics:  
A:Gene: gdhA  
A:Map position: 27 min  
C:Superfamily: glutamate dehydrogenase (NAD(P)+)  
A:Keywords: homohexamer; NADP; oxidoreductase  
F:128/Binding site: substrate (Lys) #status predicted

Query Match 47.8%; Score 1201; DB 1; Length 447;  
Best Local Similarity 54.0%; Pred. No. 2.7e-81;  
Matches 241; Conservative 67; Mismatches 128; Indels 10; Gaps 5;  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617; PMID:9278503  
A:Accession: A64936  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-447 <BLAT>  
A:Cross-references: GB:AE000271; GB:U00096; NID:g1788058; PIDN:AAC74831.1; PID:g1788059;  
A:Experimental source: strain K-12, substrain MG1655  
C:Genetics:  
A:Gene: gdhA  
A:Map position: 27 min  
C:Superfamily: glutamate dehydrogenase (NAD(P)+)  
A:Keywords: homohexamer; NADP; oxidoreductase  
F:128/Binding site: substrate (Lys) #status predicted

QY 47 VRQLLTFMKDPQEQPMQAVREAVSLQPVFEKRPEL--LPFQKQIVEPERVITFRVS 104  
Db 7 LSSFLNHVQKRDNPQTEFAQAVREVMVTTLWPLLEQNPYRQMSLLERLVEPERVITFRV 66

QY 105 WLDDAGNLQVNRGPRVQYSSAIGPYKGLRPHSPVNLISIMKFLAPFQIPKNSLTPLPMGG 164  
Db 67 WVDDRNQIQVNRVQVQYSSAIGPYKGMRFPHSPVNLISILKFLGFEQTFKNALATLPMGG 126  
QY 165 KGGSDDPDKGSDAEVNRFCQSPFMTLQRIHSVYQVDPAGDIGVGAREIGYLFGQYKRI 224  
Db 127 KGGSDDPDKGSGEVNRFQALMTLRYHLGADTDPAGDIGVGRREVGFPMAGMMKKL 186  
QY 225 TKNYTGVLTPKGQYSGSEIRPEATGYGAVLFVENVLKDGESLKGKRCIVSGAGNVAQY 284  
Db 187 SNNTACVFTGKLSFGSLIRPEATGYGLVYFTEAMLKRHGMFEGMRVSVSGSNVAQY 246  
QY 285 CAELLLEKGAIVLSLSDSGVYVPEPNTFREQLOAVQVDMKKKNSARISYKSDTAVYV 344  
Db 247 AIEKAMEFGARVITASDSSGTVVDESFTKEKLARLIEI-KASRDGRVADYAKSPGLVYL 305  
QY 345 DRRKPEWELDCQVDIAPCATONEIDEHDAELLKHGCOYVVEGANMPSTNEATHYKNKAG 404  
Db 306 EGQOPMSL--PVDIALPCATQNELDVDAHQIANGVKAQAEVDAELHHMLDIIHACVHEHGSGBQT 363  
QY 405 IICYPCGKAANAGGVAVSGLEMTQNRSLNWTREVRDKLRIMKDIYDSAM--GPSRRY 461  
Db 364 VLFAPGKAANAGGVATSGLENAQNAARLGWKAQVDAELHHMLDIIHACVHEHGSGBQT 423  
QY 462 NVDLAAGANTAGFTKVVADAVKQAV 487  
Db 424 N--VVOGANTAGFVKVADAMLAQGYI 447

RESULT 13  
F96990  
NADP-specific glutamate dehydrogenase [imported] - Clostridium acetobutylicum  
C:Species: Clostridium acetobutylicum  
C>Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
C:Accession: F96990  
R:Nolling, J.; Breton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,  
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo  
A:Reference number: A96900; MUID:21359325; PMID:21359325  
A:Accession: F96990  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-443 <KUR>  
A:Cross-references: UNIPROT:Q97L29; GB:AE001437; PIDN:AAK7813.1; PID:g15023619; GSPDB:G  
A:Experimental source: Clostridium acetobutylicum ATCC824  
C:Genetics:  
A:Gene: CAC0737  
C:Superfamily: glutamate dehydrogenase (NAD(P)+)

Query Match 47.7%; Score 1199; DB 2; Length 443;  
Best Local Similarity 54.4%; Pred. No. 3.8e-81;  
Matches 242; Conservative 69; Mismatches 122; Indels 12; Gaps 5;  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617; PMID:9278503  
A:Accession: A64936  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-447 <VAL>  
A:Experimental source: strain K12  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co  
A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617; PMID:9278503  
A:Accession: A64936  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-447 <BLAT>  
A:Cross-references: GB:AE000271; GB:U00096; NID:g1788058; PIDN:AAC74831.1; PID:g1788059;  
A:Experimental source: strain K-12, substrain MG1655  
C:Genetics:  
A:Gene: gdhA  
A:Map position: 27 min  
C:Superfamily: glutamate dehydrogenase (NAD(P)+)  
A:Keywords: homohexamer; NADP; oxidoreductase  
F:128/Binding site: substrate (Lys) #status predicted

QY 47 VRQLLTFMKDPQEQPMQAVREAVSLQPVFEKRPEL--PIFQKQIVEPERVITFRVS 104  
Db 4 LKHVMDVDVKNRPNRPFHQVKEVLLSLRIVAEKHPWAKDKIFDKIVPEPQIIFRVP 63  
QY 105 WLDDAGNLQVNRGPRVQYSSAIGPYKGLRPHSPVNLISIMKFLAPFQIPKNSLTPLPMGG 164  
Db 64 WDDNGBEHINRGPRIOFNSAIGPYKGLRPHSPVNLISIMKFLAPFQIPKNSLTPLPMGG 123  
QY 165 KGGSDDPDKGSDAEVNRFCQSPFMTLQRIHSVYQVDPAGDIGVGAREIGYLFGQYKRI 224  
Db 124 KGGSDDPDKGSDAEVNRFCQSPFMTLQRIHSVYQVDPAGDIGVGAREIGYLFGQYKRI 183  
QY 225 TKNYTGVLTPKGQYSGSEIRPEATGYGAVLFVENVLKDGESLKGKRCIVSGAGNVAQY 284  
Db 184 RNESTGVLTGKGLTGLGSLVRTEATGYGLCYFMNEALKAKGKSPDGATVVIISGSGNVAIY 243  
QY 285 CAELLLEKGAIVLSLSDSGVYVPEPNTFREQLOAVQVDMKKKNSARISYKSDTAVY 342  
Db 7 LSSFLNHVQKRDNPQTEFAQAVREVMVTTLWPLLEQNPYRQMSLLERLVEPERVITFRV 66

Db 244 ANQATQLGAKVAMSDSNGYIYDANGINLNTIRKIKEVERK-----RIHEYTKYHPNASY 299

Qy 343 VGDRRKPWELDCOVDFIAFPATONEIDEHDAELLIKHGCOYVVEGAMMPSTNEAIHKYNK 402

Db 300 TEGCDGIMWKLK--DIALPCATONEIDENSAKTLIANGCYAVCEGAMPESTIEAVDLFIK 357

Qy 403 AGLIYCPGAANAGGVAVSGLEWTONRMSLNWTRREVRDKLERIMKDIYDSAMGFSRRYN 462

Db 358 NKVIFGPAKAAAGGVATSALEMSQNSMRYSTFEEDVKLQINIMKNIYIKCSNAANEYG 417

Qy 463 VD--LAAGANAGTFTKVADAVKAQG 485

Db 418 FEDNLVAGANIAGFTKVACAMYSLG 442

RESULT 14

C90937

NADP-specific glutamate dehydrogenase [imported] - Escherichia coli (strain O157:H7, sub

C:Species: Escherichia coli

C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004

C:Accession: C90937

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ieshi, K.; Yokoyama, K.; Han, C.G.;

Gasawara, N.; Yasunaga, T.; Kuwara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno

A:Reference number: A99629; MUID:21156231; PMID:11258796

A:Accession: C90937

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-447 <HAY>

A:Cross-references: UNIPROT:Q8XDW9; GB:BA000007; PIDN:BA835890.1; PID:gr13361934; GSPDB:G

A:Experimental source: strain O157:H7, substrain RIMD 0509952

C:Genetics:

A:Gene: ECs2467

C:Superfamily: glutamate dehydrogenase (NAD(P)+)

Query Match 47.7%; Score 1198; DB 2; Length 447;

Best Local Similarity 53.8%; Pred. No. 4.6e-81;

Matches 240; Conservative 68; Mismatches 128; Indels 10; Gaps 5;

Qy 47 VRQLLTFIMKDPQEQEFMQAVREAVLSQPVFEKRPDL--LPFQKQIVEPERVITFRVS 104

Db 7 LESFLNHVQKRDPNQTEFAQAVREVMVTLWPFLEQNPKYRQMSLLERLVEPERVIOFRV 66

Qy 105 WLDAGNLQVNRGFRVQVSSAIGPYKGLRPHSPVNSIMKFLAPEQIFKNSLTTLPMGG 164

Db 67 WDDRNQVQVNRVQVSSAIGPYKGNRPHSPVNSILKFLGFEQTFKNALTTLPMGG 126

Qy 165 KGGSDFDPKGSDAEVMRFQSFMTLQRIHSYVQDVPAGDIGVGAREIGVLFQYKRI 224

Db 127 KGGSDFDPKGSSEGEVNRFCQALMTLYRHLGADTVDPAGDIGVGREVGFMAGMMKKL 186

Qy 225 TKNYTGVLTPKQEGYSGSIRPEATGYGAVLFVENVLKDGESLKGKCLVSGAGNVAQY 284

Db 187 SNTACVFTGKLSFGGSLIRPEATGYGLVYFTTEAMLKRHGMFGFMRVSVSGSGNVAQY 246

Qy 285 CAELLEKGAIVLSLSDSGYVYVNGFTREOLQAVQDMKKKNSARISEYKSDTAVYVG 344

Db 127 KGGSDFDPKGSSEGEVNRFCQALMTLYRHLGADTVDPAGDIGVGREVGFMAGMMKKL 186

Qy 225 TKNYTGVLTPKQEGYSGSIRPEATGYGAVLFVENVLKDGESLKGKCLVSGAGNVAQY 284

Db 187 SNTACVFTGKLSFGGSLIRPEATGYGLVYFTTEAMLKRHGMFGFMRVSVSGSGNVAQY 246

Qy 285 CAELLEKGAIVLSLSDSGYVYVNGFTREOLQAVQDMKKKNSARISEYKSDTAVYVG 344

Db 127 KGGSDFDPKGSSEGEVNRFCQALMTLYRHLGADTVDPAGDIGVGREVGFMAGMMKKL 186

Qy 225 TKNYTGVLTPKQEGYSGSIRPEATGYGAVLFVENVLKDGESLKGKCLVSGAGNVAQY 284

Db 187 SNTACVFTGKLSFGGSLIRPEATGYGLVYFTTEAMLKRHGMFGFMRVSVSGSGNVAQY 246

Qy 285 CAELLEKGAIVLSLSDSGYVYVNGFTREOLQAVQDMKKKNSARISEYKSDTAVYVG 344

Db 247 AIEKAMEFGARVITASDSSGTVDSESGFTKEKLARLIEI-KSSRDGRVADYAKFGLVYL 305

Qy 345 DRKPWELDCOVDFIAFPATONEIDEHDAELLIKHGCOYVVEGAMMPSTNEAIHKYNKAG 404

Db 306 EGQOPMSV--PVDIALPCATONELDVDAAHQLIANGKVAEGANMPTTIEATELFPQOAG 363

Qy 405 IYICPGKAANAGGVAVSGLEWTONRMSLNWTRREVRDKLERIMKDIYDSAM---GPSRRY 461

Db 364 VLFAPGKAANAGGVATSGLEMAQNAARLGWKAKEVDARLHMLDIHHACVHEHGEGBQT 423

Qy 462 NVDLAAGANIAGTFTKVADAVKAQGAV 487

Db 424 N--YVQGANIAGFVKVADAMLAQGV 447

RESULT 15

G85785

NADP-specific glutamate dehydrogenase [imported] - Escherichia coli (strain O157:H7, sub

C:Species: Escherichia coli

C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004

C:Accession: G85785

R:Perina, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaesner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoudis, K.; Apodaca,

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: G85785

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-447 <STO>

A:Cross-references: UNIPROT:Q8XDW9; GB:AE005174; NID:gi2515786; PIDN:AA056747.1; GSPDB:B

A:Experimental source: strain O157:H7, substrain EDJ933

C:Genetics:

A:Gene: gdhA

C:Superfamily: glutamate dehydrogenase (NAD(P)+)

Query Match 47.7%; Score 1198; DB 2; Length 447;

Best Local Similarity 53.8%; Pred. No. 4.6e-81;

Matches 240; Conservative 68; Mismatches 128; Indels 10; Gaps 5;

Qy 47 VRQLLTFIMKDPQEQEFMQAVREAVLSQPVFEKRPDL--LPFQKQIVEPERVITFRVS 104

Db 7 LESFLNHVQKRDPNQTEFAQAVREVMVTLWPFLEQNPKYRQMSLLERLVEPERVIOFRV 66

Qy 105 WLDAGNLQVNRGFRVQVSSAIGPYKGLRPHSPVNSIMKFLAPEQIFKNSLTTLPMGG 164

Db 67 WDDRNQVQVNRVQVSSAIGPYKGNRPHSPVNSILKFLGFEQTFKNALTTLPMGG 126

Qy 165 KGGSDFDPKGSDAEVMRFQSFMTLQRIHSYVQDVPAGDIGVGAREIGVLFQYKRI 224

Db 127 KGGSDFDPKGSSEGEVNRFCQALMTLYRHLGADTVDPAGDIGVGREVGFMAGMMKKL 186

Qy 225 TKNYTGVLTPKQEGYSGSIRPEATGYGAVLFVENVLKDGESLKGKCLVSGAGNVAQY 284

Db 187 SNTACVFTGKLSFGGSLIRPEATGYGLVYFTTEAMLKRHGMFGFMRVSVSGSGNVAQY 246

Qy 285 CAELLEKGAIVLSLSDSGYVYVNGFTREOLQAVQDMKKKNSARISEYKSDTAVYVG 344

Db 247 AIEKAMEFGARVITASDSSGTVDSESGFTKEKLARLIEI-KSSRDGRVADYAKFGLVYL 305

Qy 345 DRKPWELDCOVDFIAFPATONEIDEHDAELLIKHGCOYVVEGAMMPSTNEAIHKYNKAG 404

Db 306 EGQOPMSV--PVDIALPCATONELDVDAAHQLIANGKVAEGANMPTTIEATELFPQOAG 363

Qy 405 IYICPGKAANAGGVAVSGLEWTONRMSLNWTRREVRDKLERIMKDIYDSAM---GPSRRY 461

Db 364 VLFAPGKAANAGGVATSGLEMAQNAARLGWKAKEVDARLHMLDIHHACVHEHGEGBQT 423

Qy 462 NVDLAAGANIAGTFTKVADAVKAQGAV 487

Db 424 N--YVQGANIAGFVKVADAMLAQGV 447

Search completed: September 8, 2005, 02:44:38

Job time : 23.1308 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 8, 2005, 02:10:02 ; Search time 96.0793 Seconds  
(without alignments)  
1960.383 Million cell updates/sec

Title: US-10-627-886-24

Perfect score: 2513

Sequence: 1 MAVSLBEQISAMDATTGDTFT.....GANTIAGFTKVADAVKAQGA 487

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 38760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query Match | Length | ID | Description        |
|------------|--------|-------------|--------|----|--------------------|
| 1          | 2513   | 100.0       | 487    | 5  | Aau98954 Mature NA |
| 2          | 2513   | 100.0       | 487    | 8  | Adq36729 Mature NA |
| 3          | 2508   | 99.8        | 512    | 2  | Aaw15408 NADP-spec |
| 4          | 2508   | 99.8        | 512    | 5  | Aau98951 NADP-glut |
| 5          | 2508   | 99.8        | 512    | 8  | Adq36709 NADP-spec |
| 6          | 2508   | 99.8        | 526    | 2  | Aaw15407 NADP-spec |
| 7          | 2508   | 99.8        | 526    | 5  | Aau98950 NADP-glut |
| 8          | 2508   | 99.8        | 526    | 8  | Adq36707 NADP-spec |
| 9          | 2505   | 99.7        | 487    | 2  | Aaw15411 NADP-spec |
| 10         | 2465   | 98.1        | 476    | 2  | Aaw15412 NADP-spec |
| 11         | 2465   | 98.1        | 476    | 5  | Aau98955 Mature NA |
| 12         | 2465   | 98.1        | 476    | 8  | Adq36731 Mature NA |
| 13         | 1309   | 52.1        | 445    | 6  | Abu38763 Protein e |
| 14         | 1309   | 52.1        | 450    | 7  | Abu71900 Pseudomon |
| 15         | 1300.5 | 51.8        | 444    | 8  | Adp08330 Neisseria |
| 16         | 1297.5 | 51.6        | 444    | 6  | Abp77942 N. gonorr |
| 17         | 1297.5 | 51.6        | 444    | 6  | Abu37205 Protein e |
| 18         | 1294.5 | 51.5        | 444    | 5  | Aau72986 Neisseria |
| 19         | 1294.5 | 51.5        | 444    | 6  | Abu38117 Protein e |
| 20         | 1287.5 | 51.2        | 449    | 6  | Abu39614 Protein e |
| 21         | 1281   | 51.0        | 445    | 8  | Adq24914 Bacterial |
| 22         | 1259   | 50.1        | 454    | 8  | Adm27186 Bacterial |
| 23         | 1257.5 | 50.0        | 462    | 6  | Abu17276 Protein e |
| 24         | 1257.5 | 50.0        | 467    | 6  | Ada34438 Acinetoba |
| 25         | 1250.5 | 49.8        | 448    | 5  | Abp65630 Bifidobac |

#### ALIGNMENTS

##### RESULT 1

Aau98954

ID Aau98954 standard; protein; 487 AA.

AC Aau98954;

DT 24-SEP-2002 (first entry)

DE Mature NADP-glutamate dehydrogenase alpha subunit.

XX NADP-specific glutamate dehydrogenase; NADP-GDH; alpha subunit; alga;

KW nitrogen metabolism; plant; ammonium assimilation; transgenic;

KW ammonia toxicity tolerance; osmotic stress tolerance; enzyme.

OS Chlorella sorokiniana.

PN US2002062495-A1.

PD 23-MAY-2002.

PF 01-MAY-1998; 98US-00070844.

PR 01-MAY-1998; 98US-00070844.

XX (SCHM/) SCHMIDT R R.

PA (MILL/) MILLER P.

XX Schmidt RR, Miller P;

XX WPI; 2002-499691/53.

XX N-PSDB; ABK51025.

PT Transforming a plant with a polynucleotide encoding a polypeptide with glutamate dehydrogenase activity provides a plant with modulated nitrogen metabolism useful to increase yield and ammonium and osmotic stress tolerance.

XX Claim 7; Page 27-28; 35pp; English.

XX The invention relates to a method of modulating nitrogen metabolism in plant cells, comprising transcribing a plant cell with a polynucleotide encoding a polypeptide having glutamate dehydrogenase activity, and culturing the cell to produce descendant cells which express the polypeptide. The method is used to provide plants with increased yield, improved ammonium assimilation properties, increased tolerance to ammonia toxicity, improved osmotic stress tolerance and improved composition. The present sequence represents the amino acid sequence of Chlorella sorokiniana mature NADP-glutamate dehydrogenase alpha subunit, used in

|    |        |      |     |   |          |                    |
|----|--------|------|-----|---|----------|--------------------|
| 26 | 1239.5 | 49.3 | 448 | 6 | ABU29386 | Abu29386 Protein e |
| 27 | 1239.5 | 49.3 | 448 | 8 | ADH97147 | Adh97147 E. faecal |
| 28 | 1239   | 49.3 | 449 | 5 | AAU91467 | AAU91467 Haemophil |
| 29 | 1238   | 49.3 | 449 | 4 | AB88536  | AB88536 Haemophil  |
| 30 | 1238   | 49.3 | 449 | 6 | ABU30172 | ABU30172 Protein e |
| 31 | 1236.5 | 49.2 | 449 | 5 | ABP28423 | Abp28423 Streptoco |
| 32 | 1234.5 | 49.1 | 448 | 7 | ADH85999 | Adh85999 Enterococ |
| 33 | 1230.5 | 49.0 | 449 | 6 | ABU44405 | Abu44405 Protein e |
| 34 | 1230   | 48.9 | 449 | 6 | ABU38946 | Abu38946 Protein e |
| 35 | 1221   | 48.6 | 448 | 8 | ADK47974 | Adk47974 Streptoco |
| 36 | 1214   | 48.3 | 448 | 6 | ABU46100 | Abu46100 Protein e |
| 37 | 1212   | 48.2 | 448 | 6 | ABU01740 | Abu01740 S. pneumo |
| 38 | 1211.5 | 48.2 | 448 | 8 | ADH97149 | Adh97149 E. faecal |
| 39 | 1210.5 | 48.2 | 458 | 8 | ADS28251 | Adq28251 Bacterial |
| 40 | 1207.5 | 48.1 | 464 | 6 | ABU23354 | Abu23354 Protein e |
| 41 | 1205.5 | 48.0 | 424 | 6 | ADN17964 | Adn17964 Bacterial |
| 42 | 1205.5 | 48.0 | 444 | 6 | ABU20518 | Abu20518 Protein e |
| 43 | 1204   | 47.9 | 447 | 2 | AAW08092 | Aaw08092 Glutamina |
| 44 | 1201   | 47.8 | 447 | 2 | AAW60830 | Aaw60830 E. coli g |
| 45 | 1201   | 47.8 | 447 | 6 | ABU15360 | Abu15360 Protein e |



```

CC the method of the invention
XX
SQ Sequence 487 AA;

Query Match      100.0%; Score 2513; DB 5; Length 487;
Best Local Similarity 100.0%; Pred. No. 5.6e-231;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAVSLEEQISAMDATGDTALQKAVQKMATKAGTEGLVHGINKPDPVRLQLTEIFPKDPE 60
DB 1 MAVSLEEQISAMDATGDTALQKAVQKMATKAGTEGLVHGINKPDPVRLQLTEIFPKDPE 60
QY 61 QOEFMQAVREAVSLQPVFEKRPPELLPIFKQIVPEPVTFRVSWLDDAGNLQVNRGRPV 120
DB 61 QOEFMQAVREAVSLQPVFEKRPPELLPIFKQIVPEPVTFRVSWLDDAGNLQVNRGRPV 120
QY 121 QYSSAIGPYKGLRPHPSVNLISIMKFLAPEQIFKNSLTTLPMGGGKGSDPDPKGSDAE 180
DB 121 QYSSAIGPYKGLRPHPSVNLISIMKFLAPEQIFKNSLTTLPMGGGKGSDPDPKGSDAE 180
QY 181 VNRFCQSPMTLQRIHSYVDVPAGDIGVAREIGYLFQYKRITKNTVGLTPKGQBYG 240
DB 181 VNRFCQSPMTLQRIHSYVDVPAGDIGVAREIGYLFQYKRITKNTVGLTPKGQBYG 240
QY 241 GSEIRPEATGYGAVLFVENVLKDGESLKGKRCVSGAGNVAQYCAELLLKGAIVLSLS 300
DB 241 GSEIRPEATGYGAVLFVENVLKDGESLKGKRCVSGAGNVAQYCAELLLKGAIVLSLS 300
QY 301 DSQGYVYEPNGFTREQLQAVQDMKKNSARISEYKSDTAVVGGRRKRPWELDCQVDIAF 360
DB 301 DSQGYVYEPNGFTREQLQAVQDMKKNSARISEYKSDTAVVGGRRKRPWELDCQVDIAF 360
QY 361 PCATONEIDEHDAELLIKHGQYVYVEGANMPSTNEAIHKYNKAGIIPCPCAAANAGGVAV 420
DB 361 PCATONEIDEHDAELLIKHGQYVYVEGANMPSTNEAIHKYNKAGIIPCPCAAANAGGVAV 420
QY 421 SGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANTAGFTKVADA 480
DB 421 SGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANTAGFTKVADA 480
QY 481 VKAQGAV 487
DB 481 VKAQGAV 487

RESULT 3
AAW15408
ID AAW15408 standard; protein; 512 AA.
XX

```

WPI; 2004-533134/51.  
N-PSDB; ADQ36728.

Increasing or decreasing nitrogen metabolism in plant cells, for plant with increased yield and improved tolerance to ammonia toxicity and osmotic stress, by transforming plant cell with nucleic acid having glutamate dehydrogenase activity.

Claim 7; SEQ ID NO 24; 36pp; English.

The present invention relates to increasing or decreasing the nitrogen metabolism in plant cells by transforming a plant cell with a polynucleotide encoding a polypeptide having glutamate dehydrogenase (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709, ADQ36731), or their fragments, which exhibits GDH activity. The polynucleotide is operably linked to a polynucleotide encoding a chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their fragments that exhibit chloroplast transit activity. The method is useful for increasing or decreasing the nitrogen metabolism in plant cells. The methods, polynucleotides, and polypeptides are useful in producing plant with increased yield, and with improved tolerance to ammonia toxicity, osmotic stress, and composition of the crop or plant. The present sequence is the mature alpha subunit of the NADP-specific GDH used in the method of the invention.

Sequence 487 AA;

Query Match 100.0%; Score 2513; DB 8; Length 487;  
Best Local Similarity 100.0%; Pred. No. 5.6e-231;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAVSLEEQISAMDATGDTALQKAVQKMATKAGTEGLVHGINKPDPVRLQLTEIFPKDPE 60  
DB 1 MAVSLEEQISAMDATGDTALQKAVQKMATKAGTEGLVHGINKPDPVRLQLTEIFPKDPE 60  
QY 61 QOEFMQAVREAVSLQPVFEKRPPELLPIFKQIVPEPVTFRVSWLDDAGNLQVNRGRPV 120  
DB 61 QOEFMQAVREAVSLQPVFEKRPPELLPIFKQIVPEPVTFRVSWLDDAGNLQVNRGRPV 120  
QY 121 QYSSAIGPYKGLRPHPSVNLISIMKFLAPEQIFKNSLTTLPMGGGKGSDPDPKGSDAE 180  
DB 121 QYSSAIGPYKGLRPHPSVNLISIMKFLAPEQIFKNSLTTLPMGGGKGSDPDPKGSDAE 180  
QY 181 VNRFCQSPMTLQRIHSYVDVPAGDIGVAREIGYLFQYKRITKNTVGLTPKGQBYG 240  
DB 181 VNRFCQSPMTLQRIHSYVDVPAGDIGVAREIGYLFQYKRITKNTVGLTPKGQBYG 240  
QY 241 GSEIRPEATGYGAVLFVENVLKDGESLKGKRCVSGAGNVAQYCAELLLKGAIVLSLS 300  
DB 241 GSEIRPEATGYGAVLFVENVLKDGESLKGKRCVSGAGNVAQYCAELLLKGAIVLSLS 300  
QY 301 DSQGYVYEPNGFTREQLQAVQDMKKNSARISEYKSDTAVVGGRRKRPWELDCQVDIAF 360  
DB 301 DSQGYVYEPNGFTREQLQAVQDMKKNSARISEYKSDTAVVGGRRKRPWELDCQVDIAF 360  
QY 361 PCATONEIDEHDAELLIKHGQYVYVEGANMPSTNEAIHKYNKAGIIPCPCAAANAGGVAV 420  
DB 361 PCATONEIDEHDAELLIKHGQYVYVEGANMPSTNEAIHKYNKAGIIPCPCAAANAGGVAV 420  
QY 421 SGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANTAGFTKVADA 480  
DB 421 SGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANTAGFTKVADA 480  
QY 481 VKAQGAV 487  
DB 481 VKAQGAV 487

RESULT 3  
AAW15408  
ID AAW15408 standard; protein; 512 AA.  
XX

AAW15408;  
 17-OCT-2003 (revised)  
 10-JUL-1997 (first entry)  
 NADP-specific glutamate dehydrogenase beta-subunit precursor.  
 Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;  
 chloroplast; transgenic plant.  
 Chlorella sorokiniana; strain UTEX 1230.  
 W09712983-A1.  
 10-APR-1997.  
 03-OCT-1996; 96WO-US015921.  
 06-OCT-1995; 95US-00541033.  
 (UYFL) UNIV FLORIDA.  
 Schmidt RR, Miller P;  
 WPI; 1997-226226/20.  
 N-PSDB; AAT64530, AAT64543.  
 DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella  
 sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism  
 plant cells.  
 Claim 1; Page 29-32; 61pp; English.  
 2 Polypeptides (AAW15407 and AAW15408) respectively comprise the alpha  
 (AAW15407) and beta subunit (AAW15408) precursor proteins of an ammonium-  
 inducible, chloroplast-localized NADP-specific glutamate dehydrogenase  
 (NADP-GDH) of Chlorella sorokiniana. They are processed to mature alpha  
 and beta subunits (see also AAW15411-12) that comprise the active NADP-  
 GDH hexameric isoenzymes. The N metabolism of plants can be modulated  
 (pref. increasing the assimilation of inorganic N into organic N) by  
 transforming them with nucleotide sequences (see also AAT64529-30,  
 AAT64547-48) encoding the alpha and/or beta subunits or precursor  
 proteins. Such plants show improved properties, e.g. increased crop yield  
 and improved stress tolerance. Heterohexamers having alpha and beta  
 subunits can be expressed that have higher aminating/deaminating activity  
 ratios (i.e. higher capacity for glutamate synthesis) than homohexamers.  
 (Updated on 17-OCT-2003 to standardise OS field)  
 Sequence 512 AA;  
 Query Match 99.8%; Score 2508; DB 2; Length 512;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-230; Indels 0; Gaps 0;  
 Matches 486; Conservative 0; Mismatches 0;  
 2 AVSLEEQISAMDTGDTALQKAVKQWATKAGTEGLVHGKIPDVROLLTEIFMKDPEQ 61  
 27 AVSLEEQISAMDTGDTALQKAVKQWATKAGTEGLVHGKIPDVROLLTEIFMKDPEQ 86  
 62 QEFMQAVREAVSLQVPFKEKPELLPIPKQIVEPERVITFRVSLDDAGNLQVNRGFRVQ 121  
 87 QEFMQAVREAVSLQVPFKEKPELLPIPKQIVEPERVITFRVSLDDAGNLQVNRGFRVQ 146  
 122 YSSAIGPYKGLRHPSVNLSTMKFLAEQIFKNSLTLLPMGGGKGSDFDPKGSDAEV 181  
 147 YSSAIGPYKGLRHPSVNLSTMKFLAEQIFKNSLTLLPMGGGKGSDFDPKGSDAEV 206  
 182 MRFQSFMTLQRLHSYVDVPAGDIGVAREIGVLFQYKRITKNYTGVLTPKGQYGG 241  
 207 MRFQSFMTLQRLHSYVDVPAGDIGVAREIGVLFQYKRITKNYTGVLTPKGQYGG 266  
 242 SEIRPEATGYGAVLFVENVLKDGESLKGKRLVSGAGNVAQYCAELLLKGAIVLSLD 301  
 267 SEIRPEATGYGAVLFVENVLKDGESLKGKRLVSGAGNVAQYCAELLLKGAIVLSLD 326

302 SQGYVPEPNGFTREOLQAVODMKKNSARISEYKSDTAVYVGRRRKPEWELDCQVDIAPP 361  
 327 SQGYVPEPNGFTREOLQAVODMKKNSARISEYKSDTAVYVGRRRKPEWELDCQVDIAPP 386  
 362 CATONEIDEHDAELLIKHGQYVVEGANMPSTNEAIHKYNKAGIYCPGKAANAGGVAVS 421  
 387 CATONEIDEHDAELLIKHGQYVVEGANMPSTNEAIHKYNKAGIYCPGKAANAGGVAVS 446  
 422 GLEMTQNRMSLNTWREVRDKLERIMKDIYDSAMGPSRRRYNVVDLAAGANIAGFTKVADAV 481  
 447 GLEMTQNRMSLNTWREVRDKLERIMKDIYDSAMGPSRRRYNVVDLAAGANIAGFTKVADAV 506  
 482 KAQGAV 487  
 507 KAQGAV 512

RESULT 4  
 AAU98951  
 ID AAU98951 standard; protein; 512 AA.  
 AC AAU98951;  
 DT 24-SEP-2002 (first entry)  
 DE NADP-glutamate dehydrogenase beta subunit.  
 KW NADP-specific glutamate dehydrogenase; NADP-GDH; beta subunit; alga;  
 KW nitrogen metabolism; plant; ammonium assimilation; transgenic;  
 KW ammonia toxicity tolerance; osmotic stress tolerance; enzyme.  
 OS Chlorella sorokiniana.  
 PN US2002062495-A1.  
 PD 23-MAY-2002.  
 PF 01-MAY-1998; 98US-00070844.  
 PR 01-MAY-1998; 98US-00070844.  
 PA (SCHM/) SCHMIDT R R.  
 PA (MILL/) MILLER P.  
 PI Schmidt RR, Miller P;  
 WPI; 2002-499691/53.  
 DR N-PSDB; ABK51008.  
 Transforming a plant with a polynucleotide encoding a polypeptide with  
 glutamate dehydrogenase activity provides a plant with modulated nitrogen  
 metabolism useful to increase yield and ammonium and osmotic stress  
 tolerance.  
 Claim 6; Page 17-18; 35pp; English.  
 The invention relates to a method of modulating nitrogen metabolism in  
 plant cells, comprising transforming a plant cell with a polynucleotide  
 encoding a polypeptide having glutamate dehydrogenase activity, and  
 culturing the cell to produce descendant cells which express the  
 polypeptide. The method is used to provide plants with increased yield,  
 improved ammonium assimilation properties, increased tolerance to ammonia  
 toxicity, improved osmotic stress tolerance, and improved composition. The  
 present sequence represents the amino acid sequence of Chlorella  
 sorokiniana NADP-glutamate dehydrogenase beta subunit, used in the method  
 of the invention  
 Sequence 512 AA;  
 Query Match 99.8%; Score 2508; DB 5; Length 512;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-230;  
 Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 2 AVSLEEQISAMDATTGDTALQKAVQMATKAGTEGLVHGINKPDVROLLEIFPKDPEQ 61
DB 27 AVSLEEQISAMDATTGDTALQKAVQMATKAGTEGLVHGINKPDVROLLEIFPKDPEQ 86
QY 62 QEFMQAVREAVSLQPVPEKPELLPIPKQIVPERVITFRVSWLDDAGNLQVNRGPRVQ 121
DB 87 QEFMQAVREAVSLQPVPEKPELLPIPKQIVPERVITFRVSWLDDAGNLQVNRGPRVQ 146
QY 122 YSSAIGPYKGLRPHPSVNLISIMKFLAPEQIFKNSLTTLPMGGGKGGSDPDKGSDAEV 181
DB 147 YSSAIGPYKGLRPHPSVNLISIMKFLAPEQIFKNSLTTLPMGGGKGGSDPDKGSDAEV 206
QY 182 MRFQSPMTLQRIHSYVDVPAGDIGVGAREIGYLFQYKRITKNYTVGLTPKGQBYGG 241
DB 207 MRFQSPMTLQRIHSYVDVPAGDIGVGAREIGYLFQYKRITKNYTVGLTPKGQBYGG 266
QY 242 SEIRPEATGYGAVLFVENVLKDGESLKGKCLVSGAGNVAQYCAELLEKGAVLSLSD 301
DB 267 SEIRPEATGYGAVLFVENVLKDGESLKGKCLVSGAGNVAQYCAELLEKGAVLSLSD 326
QY 302 SQGYVPEPNGFTREQLQAVQDMKKNNNSARISEYKSDTAVTVGDRRKPWELDCQVDIAFP 361
DB 327 SQGYVPEPNGFTREQLQAVQDMKKNNNSARISEYKSDTAVTVGDRRKPWELDCQVDIAFP 386
QY 362 CATQNEIDEHDAELLIKHGQYVVEGANMPSTNEAIHKYNKAGIYICPGKAANAGGVAVS 421
DB 387 CATQNEIDEHDAELLIKHGQYVVEGANMPSTNEAIHKYNKAGIYICPGKAANAGGVAVS 446
QY 422 GLENTQNRMSLNWTRREEVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAV 481
DB 447 GLENTQNRMSLNWTRREEVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAV 506
QY 482 KAQGA 487
DB 507 KAQGA 512

RESULT 5
ADQ36709
ID ADQ36709 standard; protein; 512 AA.
XX
AC ADQ36709;
XX
DT 23-SEP-2004 (first entry)
XX
DE NADP-specific GDH beta subunit precursor protein, SEQ ID 4.
XX
KW Nitrogen metabolism; plant; glutamate dehydrogenase; GDH; enzyme;
KW beta subunit; NADP-specific GDH; NADP-specific glutamate dehydrogenase.
XX
OS Chlorella sorokiniana.
XX
PN US2004128710-A1.
XX
PD 01-JUL-2004.
XX
PF 24-JUL-2003; 2003US-00627886.
XX
PR 01-MAY-1998; 98US-00070844.
XX
PA (SCHM/) SCHMIDT R R.
PA (MILL/) MILLER P.
XX
PI Schmidt RR, Miller P;
XX
DR WPI; 2004-533134/51.
DR N-PSDB; ADQ36708.
XX
PT Increasing or decreasing nitrogen metabolism in plant cells, for plant
PT with increased yield and improved tolerance to ammonia toxicity and
PT osmotic stress, by transforming plant cell with nucleic acid having
PT glutamate dehydrogenase activity.

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XX Claim 7; SEQ ID NO 4; 36pp; English.
XX
CC The present invention relates to increasing or decreasing the nitrogen
CC metabolism in plant cells by transforming a plant cell with a
CC polynucleotide encoding a polypeptide having glutamate dehydrogenase
CC (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH
CC (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709,
CC ADQ36731), or their fragments, which exhibits GDH activity. The
CC polynucleotide is operably linked to a polynucleotide encoding a
CC chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their
CC fragments that exhibit chloroplast transit activity. The method is useful
CC for increasing or decreasing the nitrogen metabolism in plant cells. The
CC methods, polynucleotides, and polypeptides are useful in producing plant
CC with increased yield, and with improved tolerance to ammonia toxicity,
CC osmotic stress, and composition of the crop or plant. The present
CC sequence is the precursor protein of the beta subunit of the NADP-
CC specific GDH, which is then processed to produce the mature alpha subunit
CC of the NADP-specific GDH, used in the method of the invention.
XX
SQ Sequence 512 AA;

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Query Match          99.8%; Score 2508; DB 8; Length 512;
Best Local Similarity 100.0%; Pred. No. 1.8e-230;
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AVSLEEQISAMDATTGDTALQKAVQMATKAGTEGLVHGINKPDVROLLEIFPKDPEQ 61
DB 27 AVSLEEQISAMDATTGDTALQKAVQMATKAGTEGLVHGINKPDVROLLEIFPKDPEQ 86
QY 62 QEFMQAVREAVSLQPVPEKPELLPIPKQIVPERVITFRVSWLDDAGNLQVNRGPRVQ 121
DB 87 QEFMQAVREAVSLQPVPEKPELLPIPKQIVPERVITFRVSWLDDAGNLQVNRGPRVQ 146
QY 122 YSSAIGPYKGLRPHPSVNLISIMKFLAPEQIFKNSLTTLPMGGGKGGSDPDKGSDAEV 181
DB 147 YSSAIGPYKGLRPHPSVNLISIMKFLAPEQIFKNSLTTLPMGGGKGGSDPDKGSDAEV 206
QY 182 MRFQSPMTLQRIHSYVDVPAGDIGVGAREIGYLFQYKRITKNYTVGLTPKGQBYGG 241
DB 207 MRFQSPMTLQRIHSYVDVPAGDIGVGAREIGYLFQYKRITKNYTVGLTPKGQBYGG 266
QY 242 SEIRPEATGYGAVLFVENVLKDGESLKGKCLVSGAGNVAQYCAELLEKGAVLSLSD 301
DB 267 SEIRPEATGYGAVLFVENVLKDGESLKGKCLVSGAGNVAQYCAELLEKGAVLSLSD 326
QY 302 SQGYVPEPNGFTREQLQAVQDMKKNNNSARISEYKSDTAVTVGDRRKPWELDCQVDIAFP 361
DB 327 SQGYVPEPNGFTREQLQAVQDMKKNNNSARISEYKSDTAVTVGDRRKPWELDCQVDIAFP 386
QY 362 CATQNEIDEHDAELLIKHGQYVVEGANMPSTNEAIHKYNKAGIYICPGKAANAGGVAVS 421
DB 387 CATQNEIDEHDAELLIKHGQYVVEGANMPSTNEAIHKYNKAGIYICPGKAANAGGVAVS 446
QY 422 GLENTQNRMSLNWTRREEVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAV 481
DB 447 GLENTQNRMSLNWTRREEVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAV 506
QY 482 KAQGA 487
DB 507 KAQGA 512

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RESULT 6
AAW15407
ID AAW15407 standard; protein; 526 AA.
XX
AC AAW15407;
XX
DT 17-OCT-2003 (revised)
DT 10-JUL-1997 (first entry)
XX
DE NADP-specific glutamate dehydrogenase alpha-subunit precursor.

```

XX Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;  
 KW chloroplast; transgenic plant.  
 XX  
 OS Chlorella sorokiniana; strain UTEX 1230.  
 XX  
 PN WO9712983-Al.  
 XX  
 PD 10-APR-1997.  
 XX  
 XX 03-OCT-1996; 96WO-US015921.  
 XX  
 XX 06-OCT-1995; 95US-00541033.  
 XX  
 XX (UYFL ) UNIV FLORIDA.  
 XX  
 XX Schmidt RR, Miller P;  
 XX  
 XX WPI: 1997-226226/20.  
 DR  
 DR N-PSDB; AAT64529, AAT64542.  
 XX  
 XX DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella  
 PT sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism  
 PT plant cells.  
 XX  
 XX Claim 1; Page 25-27; 61pp; English.  
 XX  
 XX 2 Polypeptides (AAW15407 and AAW15408) respectively comprise the alpha  
 CC (AAW15407) and beta subunit (AAW15408) precursor proteins of an ammonium-  
 CC inducible, chloroplast-localised NADP-specific glutamate dehydrogenase  
 CC (NADP-GDH) of Chlorella sorokiniana. They are processed to mature alpha  
 CC and beta subunits (see also AAW15411-12) that comprise the active NADP-  
 CC GDH hexameric isoenzymes. The N metabolism of plants can be modulated  
 CC (pref. increasing the assimilation of inorganic N into organic N) by  
 CC transforming them with nucleotide sequences (see also AAT64529-30,  
 CC AAT64547-48) encoding the alpha and/or beta subunits or precursor  
 CC proteins. Such plants show improved properties, e.g. increased crop yield  
 CC and improved stress tolerance. Heterohexamers having alpha and beta  
 CC subunits can be expressed that have higher aminating/deaminating activity  
 CC ratios (i.e. higher capacity for glutamate synthesis) than homoexamers.  
 CC (Updated on 17-OCT-2003 to standardise OS field)  
 XX  
 XX Sequence 526 AA;  
 SQ  
 Query Match 99.8%; Score 2508; DB 2; Length 526;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-230; Indels 0; Gaps 0;  
 Matches 486; Conservative 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0;  
 2 AVSLEEQISAMDATTGDTALQKAVKQMATKAGTEGLVHGIRKPNPDRQLLTFIFMKDPEQ 61  
 41 AVSLEEQISAMDATTGDTALQKAVKQMATKAGTEGLVHGIRKPNPDRQLLTFIFMKDPEQ 100  
 62 QEFMQAVREVAVSLQVPEKRPPELLPIFQIUEPERVITFRVSWLDDAGNLQVNRGRVQ 121  
 101 QEFMQAVREVAVSLQVPEKRPPELLPIFQIUEPERVITFRVSWLDDAGNLQVNRGRVQ 160  
 122 YSSALGPYKGGURFHPNSVNLSTMKFLAFQIIFKNSITLTPMGCGGSGDFDPKGSDAEV 181  
 161 YSSALGPYKGGURFHPNSVNLSTMKFLAFQIIFKNSITLTPMGCGGSGDFDPKGSDAEV 220  
 182 MRFCSQFMTLQHRHSYVDVDPAGDIGVGARIGVLFQYKRTIKNYTGLVLPKQGEYGG 241  
 221 MRFCSQFMTLQHRHSYVDVDPAGDIGVGARIGVLFQYKRTIKNYTGLVLPKQGEYGG 280  
 242 SEIRPEATGYGAVLFVENVLKDGSLSKGRCLVSGAGNVAQYCAELLEKGAIVLSLSD 301  
 281 SEIRPEATGYGAVLFVENVLKDGSLSKGRCLVSGAGNVAQYCAELLEKGAIVLSLSD 340  
 302 SQGYVEPNFGFTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPEWELDCQVDIAPP 361  
 341 SQGYVEPNFGFTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPEWELDCQVDIAPP 400  
 362 CATONEIDEHDAELLIKHGCCQYVVEGANPSTNEAIHKYNKAGIITPCGKAANAGGVAVS 421

Db 401 CATONEIDEHDAELLIKHGCCQYVVEGANPSTNEAIHKYNKAGIITPCGKAANAGGVAVS 460  
 QY 422 GLEMTQNRMSLNWTRREVRDKLERIMKOIYDSAMGPSREYNYDLAAGANIAGFTKVADAV 481  
 Db 461 GLEMTQNRMSLNWTRREVRDKLERIMKOIYDSAMGPSREYNYDLAAGANIAGFTKVADAV 520  
 QY 482 KAQGAV 487  
 Db 521 KAQGAV 526  
 RESULT 7  
 AAU98950  
 ID AAU98950 standard; protein; 526 AA.  
 XX  
 AC AAU98950;  
 XX  
 DT 24-SEP-2002 (first entry)  
 XX  
 DE NADP-glutamate dehydrogenase alpha subunit.  
 XX  
 KW NADP-specific glutamate dehydrogenase; NADP-GDH; alpha subunit; alga;  
 KW nitrogen metabolism; plant; ammonium assimilation; transgenic;  
 KW ammonia toxicity tolerance; osmotic stress tolerance; enzyme.  
 XX  
 OS Chlorella sorokiniana.  
 XX  
 PN US2002062495-Al.  
 XX  
 PD 23-MAY-2002.  
 XX  
 PF 01-MAY-1998; 98US-00070844.  
 XX  
 PR 01-MAY-1998; 98US-00070844.  
 XX  
 XX (SCHM/) SCHMIDT R R.  
 PA (MILL/) MILLER P.  
 PI Schmidt RR, Miller P;  
 XX  
 XX WPI: 2002-499691/53.  
 XX N-PSDB; ABK51007.  
 XX  
 PT Transforming a plant with a polynucleotide encoding a polypeptide with  
 PT glutamate dehydrogenase activity provides a plant with modulated nitrogen  
 PT metabolism useful to increase yield and ammonium and osmotic stress  
 PT tolerance.  
 XX  
 XX Claim 6; Page 13-15; 35pp; English.  
 XX  
 CC The invention relates to a method of modulating nitrogen metabolism in  
 CC plant cells, comprising transforming a plant cell with a polynucleotide  
 CC encoding a polypeptide having glutamate dehydrogenase activity, and  
 CC culturing the cell to produce descendant cells which express the  
 CC polypeptide. The method is used to provide plants with increased yield,  
 CC improved ammonium assimilation properties, increased tolerance to ammonia  
 CC toxicity, improved osmotic stress tolerance and improved composition. The  
 CC present sequence represents the amino acid sequence of Chlorella  
 CC sorokiniana NADP-glutamate dehydrogenase alpha subunit, used in the  
 CC method of the invention  
 XX  
 SQ Sequence 526 AA;  
 Query Match 99.8%; Score 2508; DB 5; Length 526;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-230; Indels 0; Gaps 0;  
 Matches 486; Conservative 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0;  
 2 AVSLEEQISAMDATTGDTALQKAVKQMATKAGTEGLVHGIRKPNPDRQLLTFIFMKDPEQ 61  
 41 AVSLEEQISAMDATTGDTALQKAVKQMATKAGTEGLVHGIRKPNPDRQLLTFIFMKDPEQ 100  
 62 QEFMQAVREVAVSLQVPEKRPPELLPIFQIUEPERVITFRVSWLDDAGNLQVNRGRVQ 121

Db 101 QSFQAVREAVSLQVPFKEPELLPIKQIVPEPVRITFRVSLDDAGNLQVNGFRVQ 160  
Qy 122 YSASATGPKYKGLRPHPSVNLSTMKFLAFQIIFKNSLTTLPMGGGKGGSDPDPKGSDAEV 181  
Db 161 YSASATGPKYKGLRPHPSVNLSTMKFLAFQIIFKNSLTTLPMGGGKGGSDPDPKGSDAEV 220  
Qy 182 MRCQSPMTLQRLHISYVQDVDPAGDIGVGAREIGVLFQYKRIITKNYTGVLTPKQEGVG 241  
Db 221 MRCQSPMTLQRLHISYVQDVDPAGDIGVGAREIGVLFQYKRIITKNYTGVLTPKQEGVG 280  
Qy 242 SEIRPEATGYGAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLKGAIVLSLSD 301  
Db 281 SEIRPEATGYGAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLKGAIVLSLSD 340  
Qy 302 SQGYVEPNPFGTRBQLQAVQDMKKNSARISEYKSDTAIVYVGGRRKPEWELDCQVDIAPP 361  
Db 341 SQGYVEPNPFGTRBQLQAVQDMKKNSARISEYKSDTAIVYVGGRRKPEWELDCQVDIAPP 400  
Qy 362 CATONEIDEHDAELLIKHGCGQYVVGANMPSTNEAIHKYNKAGIICPGKAANAGGVAVS 421  
Db 401 CATONEIDEHDAELLIKHGCGQYVVGANMPSTNEAIHKYNKAGIICPGKAANAGGVAVS 460  
Qy 422 GLEMTQNRMSLNTWTRREVRDKLERIMKOIYDSAMGPSRRYVNDLAAGANIAGFTKVADAV 481  
Db 461 GLEMTQNRMSLNTWTRREVRDKLERIMKOIYDSAMGPSRRYVNDLAAGANIAGFTKVADAV 520  
Qy 482 KAQGA 487  
Db 521 KAQGA 526

RESULT 8  
ID ADQ36707 standard; protein; 526 AA.  
XX  
AC ADQ36707;  
DT 23-SEP-2004 (first entry)  
XX  
DE NADP-specific GDH alpha subunit precursor protein, SEQ ID 2.  
XX  
KW Nitrogen metabolism; plant; glutamate dehydrogenase; GDH; enzyme;  
KW alpha subunit; NADP-specific GDH; NADP-specific glutamate dehydrogenase.  
XX  
OS Chlorella sorokiniana.  
XX  
PN US2004128710-A1.  
XX  
PD 01-JUL-2004.  
XX  
PF 24-JUL-2003; 2003US-00627886.  
XX  
PR 01-MAY-1998; 98US-00070844.  
XX  
PA (SCHM/) SCHMIDT R R.  
PA (MILL/) MILLER P.  
XX  
PI Schmidt RR, Miller P;  
XX  
XX WPI; 2004-533134/51.  
DR N-PSDB; ADQ36706.  
XX  
PT Increasing or decreasing nitrogen metabolism in plant cells, for plant  
PT with increased yield and improved tolerance to ammonia toxicity and  
PT osmotic stress, by transforming plant cell with nucleic acid having  
PT glutamate dehydrogenase activity.  
XX  
PS Claim 7; SEQ ID NO 2; 36pp; English.  
XX  
CC The present invention relates to increasing or decreasing the nitrogen  
CC metabolism in plant cells by transforming a plant cell with a  
CC polynucleotide encoding a polypeptide having glutamate dehydrogenase

CC (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH  
CC (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709,  
CC ADQ36731), or their fragments, which exhibits GDH activity. The  
CC polynucleotide is operably linked to a polynucleotide encoding a  
CC chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their  
CC fragments that exhibit chloroplast transit activity. The method is useful  
CC for increasing or decreasing the nitrogen metabolism in plant cells. The  
CC methods, polynucleotides, and polypeptides are useful in producing plant  
CC with increased yield, and with improved tolerance to ammonia toxicity,  
CC osmotic stress, and composition of the crop or plant. The present  
CC sequence is the precursor protein of the alpha subunit of the NADP-  
CC specific GDH, which is then processed to produce the mature alpha subunit  
CC of the NADP-specific GDH, used in the method of the invention.  
XX  
SQ Sequence 526 AA;  
Query Match 99.8%; Score 2508; DB 8; Length 526;  
Best Local Similarity 100.0%; Pred. No. 1.9e-230;  
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 AVSLEEQISAMDATTGDTALQKAVQKMATKAGTEGLVHGINKPDVROLLTEIFMKDPEQ 61  
Db 41 AVSLEEQISAMDATTGDTALQKAVQKMATKAGTEGLVHGINKPDVROLLTEIFMKDPEQ 100  
Qy 62 QEFMQAVREVAVSLQVPFKEPELLPIKQIVPEPVRITFRVSLDDAGNLQVNGFRVQ 121  
Db 101 QEFMQAVREVAVSLQVPFKEPELLPIKQIVPEPVRITFRVSLDDAGNLQVNGFRVQ 160  
Qy 122 YSSAIGPYKGLRPHPSVNLSTMKFLAFQIIFKNSLTTLPMGGGKGGSDPDPKGSDAEV 181  
Db 161 YSSAIGPYKGLRPHPSVNLSTMKFLAFQIIFKNSLTTLPMGGGKGGSDPDPKGSDAEV 220  
Qy 182 MRCQSPMTLQRLHISYVQDVDPAGDIGVGAREIGVLFQYKRIITKNYTGVLTPKQEGVG 241  
Db 221 MRCQSPMTLQRLHISYVQDVDPAGDIGVGAREIGVLFQYKRIITKNYTGVLTPKQEGVG 280  
Qy 242 SEIRPEATGYGAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLKGAIVLSLSD 301  
Db 281 SEIRPEATGYGAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLLKGAIVLSLSD 340  
Qy 302 SQGYVEPNPFGTRBQLQAVQDMKKNSARISEYKSDTAIVYVGGRRKPEWELDCQVDIAPP 361  
Db 341 SQGYVEPNPFGTRBQLQAVQDMKKNSARISEYKSDTAIVYVGGRRKPEWELDCQVDIAPP 400  
Qy 362 CATONEIDEHDAELLIKHGCGQYVVGANMPSTNEAIHKYNKAGIICPGKAANAGGVAVS 421  
Db 401 CATONEIDEHDAELLIKHGCGQYVVGANMPSTNEAIHKYNKAGIICPGKAANAGGVAVS 460  
Qy 422 GLEMTQNRMSLNTWTRREVRDKLERIMKOIYDSAMGPSRRYVNDLAAGANIAGFTKVADAV 481  
Db 461 GLEMTQNRMSLNTWTRREVRDKLERIMKOIYDSAMGPSRRYVNDLAAGANIAGFTKVADAV 520  
Qy 482 KAQGA 487  
Db 521 KAQGA 526  
RESULT 9  
AAW15411  
ID AAW15411 standard; protein; 487 AA.  
XX  
AC AAW15411;  
XX  
DT 17-OCT-2003 (revised)  
DT 10-JUL-1997 (first entry)  
XX  
DE NADP-specific glutamate dehydrogenase alpha subunit.  
XX  
KW Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;  
KW Chloroplast; transgenic plant.  
XX  
OS Chlorella sorokiniana; strain UTEX 1230.  
XX

PN WO9712983-A1.  
 XX 10-APR-1997.  
 XX 03-OCT-1996; 96WO-US015921.  
 XX 06-OCT-1995; 95US-00541033.  
 XX (UYFL ) UNIV FLORIDA.  
 PA Schmidt RR, Miller P;  
 PI WPI; 1997-226226/20.  
 DR N-PSDB; AAT64547.  
 XX  
 PT DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella  
 PT sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism  
 PT plant cells.  
 XX  
 PS Claim 1; Page 44-46; 61pp; English.  
 XX  
 CC 2 Polypeptides (AAW15411 and AAW15412) respectively comprise the mature  
 CC alpha subunit (AAW15407) and beta subunit (AAW15408) proteins of an  
 CC ammonium-inducible, chloroplast-localised hexameric NADP-specific  
 CC glutamate dehydrogenase (NADP-GDH) isoenzymes of Chlorella sorokiniana.  
 CC They are produced by removal of transit peptides from the precursor  
 CC proteins (AAW15407-08). The N metabolism of plants can be modulated  
 CC (pref. increasing the assimilation of inorganic N into organic N) by  
 CC transforming them with nucleotide sequences (see also AAT64529-30,  
 CC AAT64547-48) encoding the alpha and/or beta subunits or precursor  
 CC proteins. Such plants show improved properties, e.g. increased crop yield  
 CC and improved stress tolerance. Heterohexamers having alpha and beta  
 CC subunits can be expressed that have higher aminating/deaminating activity  
 CC ratios (i.e. higher capacity for glutamate synthesis) than homohexamers.  
 CC (Updated on 17-OCT-2003 to standardise OS field)  
 XX  
 SQ Sequence 487 AA;  
 Query Match 99.7%; Score 2505; DB 2; Length 487;  
 Best Local Similarity 99.8%; Pred. No. 3.3e-230;  
 Matches 486; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MAVSLEEQISAMDATGDTALQKAVQKMATKAGTEGLVHGINKPDPVRLLETFMKDPE 60  
 DB 1 MAVSLEEQISAMDATGDTALQKAVQKMATKAGTEGLVHGINKPDPVRLLETFMKDPE 60  
 QY 61 QOEFMQAVREVAVSLOPVEKPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGRV 120  
 DB 61 QOEFMQAVREVAVSLOPVEKPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGRV 120  
 QY 121 QYSSAIGPYKGLRPHPSVNLSTMKFLAPEQIFKNSLTTLPMGGGKGGSDFPKGSDAE 180  
 DB 121 QYSSAIGPYKGLRPHPSVNLSTMKFLAPEQIFKNSLTTLPMGGGKGGSDFPKGSDAE 180  
 QY 181 VNRFCQSFMTLQRIHSYVDVPAGDIGVAREIGYLFQYKXITKNTYGVLTTPKQYEVG 240  
 DB 181 VNRFCQSFMTLQRIHSYVDVPAGDIGVAREIGYLFQYKXITKNTYGVLTTPKQYEVG 240  
 QY 241 GSEIRPEATGYGAVLNVENLXDKESLKGKCLVSGAGNVAQYCAELLLEGAIVLSL 300  
 DB 241 GSEIRPEATGYGAVLNVENLXDKESLKGKCLVSGAGNVAQYCAELLLEGAIVLSL 300  
 QY 301 DSQGYVYEPNGFTREQLQAVQDMKKNSARISEYKSDTAVYVGRRKPEWELDCQVDIAF 360  
 DB 301 DSQGYVYEPNGFTREQLQAVQDMKKNSARISEYKSDTAVYVGRRKPEWELDCQVDIAF 360  
 QY 361 PCATQNEIDEHDAELLIKHGQCYVVEGANMPSTNEAIHKYNKAGIYICPGKAANAGGVAV 420  
 DB 361 PCATQNEIDEHDAELLIKHGQCYVVEGANMPSTNEAIHKYNKAGIYICPGKAANAGGVAV 420  
 QY 421 SGLEMTQNRMSLNWTRREVRDKLERIMKDIYSANGPSRRYVNDLAAGNIAAGFTKVADA 480  
 DB 421 SGLEMTQNRMSLNWTRREVRDKLERIMKDIYSANGPSRRYVNDLAAGNIAAGFTKVADA 480

QY 481 VKAQGAV 487  
 DB 481 VKAQGAV 487  
 RESULT 10  
 AAW15412  
 ID AAW15412 standard; protein; 476 AA.  
 XX  
 AC AAW15412;  
 XX  
 DT 17-OCT-2003 (revised)  
 DT 10-JUL-1997 (first entry)  
 XX  
 DE NADP-specific glutamate dehydrogenase beta subunit.  
 KW Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;  
 KW chloroplast; transgenic plant.  
 XX  
 OS Chlorella sorokiniana; strain UTEX 1230.  
 XX  
 PN WO9712983-A1.  
 PD 10-APR-1997.  
 XX  
 PF 03-OCT-1996; 96WO-US015921.  
 XX  
 PR 06-OCT-1995; 95US-00541033.  
 XX  
 PA (UYFL ) UNIV FLORIDA.  
 PI Schmidt RR, Miller P;  
 XX  
 DR WPI; 1997-226226/20.  
 DR N-PSDB; AAT64548.  
 XX  
 PT DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella  
 PT sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism  
 PT plant cells.  
 XX  
 PS Claim 1; Page 48-50; 61pp; English.  
 XX  
 CC 2 Polypeptides (AAW15411 and AAW15412) respectively comprise the mature  
 CC alpha subunit (AAW15407) and beta subunit (AAW15408) proteins of an  
 CC ammonium-inducible, chloroplast-localised hexameric NADP-specific  
 CC glutamate dehydrogenase (NADP-GDH) isoenzymes of Chlorella sorokiniana.  
 CC They are produced by removal of transit peptides from the precursor  
 CC proteins (AAW15407-08). The N metabolism of plants can be modulated  
 CC (pref. increasing the assimilation of inorganic N into organic N) by  
 CC transforming them with nucleotide sequences (see also AAT64529-30,  
 CC AAT64547-48) encoding the alpha and/or beta subunits or precursor  
 CC proteins. Such plants show improved properties, e.g. increased crop yield  
 CC and improved stress tolerance. Heterohexamers having alpha and beta  
 CC subunits can be expressed that have higher aminating/deaminating activity  
 CC ratios (i.e. higher capacity for glutamate synthesis) than homohexamers.  
 CC (Updated on 17-OCT-2003 to standardise OS field)  
 XX  
 SQ Sequence 476 AA;  
 Query Match 98.1%; Score 2465; DB 2; Length 476;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-226;  
 Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 12 MDATTGDTALQKAVQKMATKAGTEGLVHGINKPDPVRLLETFMKDPEQEFMQAVREV 71  
 DB 1 MDATTGDTALQKAVQKMATKAGTEGLVHGINKPDPVRLLETFMKDPEQEFMQAVREV 60  
 QY 72 AVSLQPVPEKPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGRVYSSAIGPYKG 131  
 DB 61 AVSLQPVPEKPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGRVYSSAIGPYKG 120  
 QY 132 GLRPHPSVNLSTMKFLAPEQIFKNSLTTLPMGGGKGGSDFPKGSDAEVMRQCFSFMT 191



Db 121 GLRFHPSVNLIMKFLAPEQIFKNSLTTLPMGGKGSGDFDPKGSDAEVMRFQSPFTE 180  
 QY 192 LQRHSIVQDVDPAGDIGVAREIGVLPQYKRIITKNTYTGVLTPKQGYGSGSIRPEATGY 251  
 Db 181 LQRHSIVQDVDPAGDIGVAREIGVLPQYKRIITKNTYTGVLTPKQGYGSGSIRPEATGY 240  
 QY 252 GAVLFVENVLKDKGSLKGRCLVSGAGNVAQYCAELLLKGAIVLSLSDSQGYVYEPNG 311  
 Db 241 GAVLFVENVLKDKGSLKGRCLVSGAGNVAQYCAELLLKGAIVLSLSDSQGYVYEPNG 300  
 QY 312 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGGDRRKPWELDCQVDIAFPCCATQNEIDEH 371  
 Db 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGGDRRKPWELDCQVDIAFPCCATQNEIDEH 360  
 QY 372 DAELLIKHGCCQYVVEGANMPSTNEAIHKYNKAGIICPGKAANAGGAVVSGLEMTQNRMS 431  
 Db 361 DAELLIKHGCCQYVVEGANMPSTNEAIHKYNKAGIICPGKAANAGGAVVSGLEMTQNRMS 420  
 QY 432 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGAV 487  
 Db 421 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGAV 476

## RESULT 11

AAU98955  
 ID AAU98955 standard; protein; 476 AA.  
 XX  
 AC AAU98955;  
 XX  
 DT 24-SEP-2002 (first entry)  
 XX  
 DE Mature NADP-glutamate dehydrogenase beta subunit.  
 XX  
 KW NADP-specific glutamate dehydrogenase; NADP-GDH; beta subunit; alga;  
 KW nitrogen metabolism; plant; ammonium assimilation; transgenic;  
 KW ammonia toxicity tolerance; osmotic stress tolerance; enzyme.  
 XX  
 OS Chlorella sorokiniana.

US2002062495-A1.

23-MAY-2002.

01-MAY-1998; 98US-00070844.

01-MAY-1998; 98US-00070844.

(SCHM/) SCHMIDT R R.  
(MILL/) MILLER P.

Schmidt RR, Miller P;

WPI; 2002-499691/53.

N-PSDB; ABK51026.

Transforming a plant with a polynucleotide encoding a polypeptide with  
 glutamate dehydrogenase activity provides a plant with modulated nitrogen  
 metabolism useful to increase yield and ammonium and osmotic stress  
 tolerance.

Claim 7; Page 31-32; 35pp; English.

The invention relates to a method of modulating nitrogen metabolism in  
 plant cells, comprising transforming a plant cell with a polynucleotide  
 encoding a polypeptide having glutamate dehydrogenase activity, and  
 culturing the cell to produce descendant cells which express the  
 polypeptide. The method is used to provide plants with increased yield,  
 improved ammonium assimilation properties, increased tolerance to ammonia  
 toxicity, improved osmotic stress tolerance and improved composition. The  
 present sequence represents the amino acid sequence of Chlorella  
 sorokiniana mature NADP-glutamate dehydrogenase beta subunit, used in the  
 method of the invention

XX Sequence 476 AA;  
 SQ  
 Query Match 98.1%; Score 2465; DB 5; Length 476;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-226;  
 Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 12 MDATGDDTALQKAVKQMATKAGTEGLVHGILKNPDVROLLTEIFMKDQEQEFMQAVREV 71  
 Db 1 MDATGDDTALQKAVKQMATKAGTEGLVHGILKNPDVROLLTEIFMKDQEQEFMQAVREV 60  
 QY 72 AVSLQPVPEKPELLPIFKQIVPEPVTTFRVSWLDDAGNLQVNRGRFVQYSSAIGPYKG 131  
 Db 61 AVSLQPVPEKPELLPIFKQIVPEPVTTFRVSWLDDAGNLQVNRGRFVQYSSAIGPYKG 120  
 QY 132 GLRFHPSVNLIMKFLAPEQIFKNSLTTLPMGGKGSGSDPDPKGSDAEVMRFQSPFTE 191  
 Db 121 GLRFHPSVNLIMKFLAPEQIFKNSLTTLPMGGKGSGSDPDPKGSDAEVMRFQSPFTE 180  
 QY 192 LQRHSIVQDVDPAGDIGVAREIGVLPQYKRIITKNTYTGVLTPKQGYGSGSIRPEATGY 251  
 Db 181 LQRHSIVQDVDPAGDIGVAREIGVLPQYKRIITKNTYTGVLTPKQGYGSGSIRPEATGY 240  
 QY 252 GAVLFVENVLKDKGSLKGRCLVSGAGNVAQYCAELLLKGAIVLSLSDSQGYVYEPNG 311  
 Db 241 GAVLFVENVLKDKGSLKGRCLVSGAGNVAQYCAELLLKGAIVLSLSDSQGYVYEPNG 300  
 QY 312 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGGDRRKPWELDCQVDIAFPCCATQNEIDEH 371  
 Db 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGGDRRKPWELDCQVDIAFPCCATQNEIDEH 360  
 QY 372 DAELLIKHGCCQYVVEGANMPSTNEAIHKYNKAGIICPGKAANAGGAVVSGLEMTQNRMS 431  
 Db 361 DAELLIKHGCCQYVVEGANMPSTNEAIHKYNKAGIICPGKAANAGGAVVSGLEMTQNRMS 420  
 QY 432 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGAV 487  
 Db 421 LNWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQGAV 476

## RESULT 12

ADQ36731

ID ADQ36731 standard; protein; 476 AA.

AC ADQ36731;

XX  
 DT 23-SEP-2004 (first entry)

DE Mature NADP-specific GDH beta subunit, SEQ ID 26.

XX Nitrogen metabolism; plant; glutamate dehydrogenase; GDH; enzyme;  
 KW beta subunit; NADP-specific GDH; NADP-specific glutamate dehydrogenase.

XX Chlorella sorokiniana.

XX US2004128710-A1.

XX 01-JUL-2004.

XX 24-JUL-2003; 2003US-00627886.

XX 01-MAY-1998; 98US-00070844.

XX (SCHM/) SCHMIDT R R.  
 XX (MILL/) MILLER P.

XX Schmidt RR, Miller P;

XX WPI; 2004-533134/51.

XX DR N-PSDB; ADQ36730.

XX Increasing or decreasing nitrogen metabolism in plant cells, for plant  
 PT with increased yield and improved tolerance to ammonia toxicity and



PT osmotic stress, by transforming plant cell with nucleic acid having  
PT glutamate dehydrogenase activity.  
XX  
PS Claim 7; SEQ ID NO 26; 36pp; English.  
XX  
CC The present invention relates to increasing or decreasing the nitrogen  
CC metabolism in plant cells by transforming a plant cell with a  
CC polynucleotide encoding a polypeptide having glutamate dehydrogenase  
CC (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH  
CC (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709,  
CC ADQ36731), or their fragments, which exhibits GDH activity. The  
CC polynucleotide is operably linked to a polynucleotide encoding a  
CC chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their  
CC fragments that exhibit chloroplast transit activity. The method is useful  
CC for increasing or decreasing the nitrogen metabolism in plant cells. The  
CC methods, polynucleotides, and polypeptides are useful in producing plant  
CC with increased yield, and with improved tolerance to ammonia toxicity,  
CC osmotic stress, and composition of the crop or plant. The present  
CC sequence is the mature beta subunit of the NADP-specific GDH used in the  
CC method of the invention.  
XX  
SQ Sequence 476 AA;

Query Match 98.1%; Score 2465; DB 8; Length 476;  
Best Local Similarity 100.0%; Pred. No. 2.1e-226; Indels 0; Gaps 0;  
Matches 476; Conservative 0; Mismatches 0;  
QY 12 MDATGDTALQKAVQKMATKAGTEGLVHGINKNPVRLTLTIFMKDPEQQFMAVREV 71  
Db 1 MDATGDTALQKAVQKMATKAGTEGLVHGINKNPVRLTLTIFMKDPEQQFMAVREV 60  
QY 72 AVSLQPVFKRPPELLIPKQIVPEPVTIFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 131  
Db 61 AVSLQPVFKRPPELLIPKQIVPEPVTIFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120  
QY 132 GLRPHPSVNLSTMKFLAPQIFKNSLTITLPMGGKGGSDFDPKGSDAEVWRFQCSFWTE 191  
Db 121 GLRPHPSVNLSTMKFLAPQIFKNSLTITLPMGGKGGSDFDPKGSDAEVWRFQCSFWTE 180  
QY 192 LQRHSYVDVPAGDIGVAREIGVLFQYKRTKNYTGVLTPKQEGVGGSEIRPEATGY 251  
Db 181 LQRHSYVDVPAGDIGVAREIGVLFQYKRTKNYTGVLTPKQEGVGGSEIRPEATGY 240  
QY 252 GAVLFVENVLKDGSLSKGRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQYVYEPNG 311  
Db 241 GAVLFVENVLKDGSLSKGRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQYVYEPNG 300  
QY 312 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAPPQATQNEIDEH 371  
Db 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAPPQATQNEIDEH 360  
QY 372 DAELLIKHGQCVVVEGANMPSNEAIHKYNKAGIYCPCGANAGGAVVSGLEMTQNRMS 431  
Db 361 DAELLIKHGQCVVVEGANMPSNEAIHKYNKAGIYCPCGANAGGAVVSGLEMTQNRMS 420  
QY 432 LNWTRREVRDKLERIMKDIYDSAMGFSRRYNDLAAGANIAGTFTKVDAAVKAQGA 487  
Db 421 LNWTRREVRDKLERIMKDIYDSAMGFSRRYNDLAAGANIAGTFTKVDAAVKAQGA 476

RESULT 13  
ABU38763  
ID ABU38763 standard; protein; 445 AA.  
XX  
AC ABU38763;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #24290.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Pseudomonas aeruginosa.

XX WO200277183-A2.  
XX PD 03-OCT-2002.  
XX PF 21-MAR-2002; 2002WO-US009107.  
XX PR 21-MAR-2001; 2001US-00815242.  
XX PR 06-SEP-2001; 2001US-00948993.  
XX PR 25-OCT-2001; 2001US-0342923P.  
XX PR 08-FEB-2002; 2002US-00072851.  
XX PR 06-MAR-2002; 2002US-0362699P.  
XX PA (ELIT-) ELITRA PHARM INC.  
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX WPI; 2003-029926/02.  
XX DR N-PSDB; ACA42633.  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 66687; 1766pp; English.  
XX  
CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 445 AA;

Query Match 52.1%; Score 1309; DB 6; Length 445;  
Best Local Similarity 59.2%; Pred. No. 7.7e-116; Indels 6; Gaps 4;  
Matches 263; Conservative 55; Mismatches 120;  
QY 47 VRLLEIFMKDPQEQFMAVREVAVSLQVFKRPELLP--IFKQIVPEPVTIFRV 104  
Db 5 VDAFLERLKRDPDQPEFHQAVEVLRSLWFLFLEANPHYLEAGIIEVERAILFRVP 64  
QY 105 WLDAGNLQVNRGFRVQYSSAIGPYKGLRPHPSVNLSTMKFLAPQIFKNSLTITLPMGG 164  
Db 65 WDDQGRVVRNVRGVQMSAIGPYKGLRPHPSVNLSTMKFLAPQIFKNSLTITLPMGG 124

QY 165 GKGSDFDPKGSDAEVMRFQSPFMTLQRIHSYVQDVDPAGDVGAREIGYLFQYKRI 224  
 Db 125 GKGSDFDPKGSDAEVMRFQSPFMTLQRIHSYVQDVDPAGDVGAREIGYLFQYKRI 184  
 QY 225 TKNYTVLTPKQYGGSEIRPEATGYGAVLVFNVLKDKGSLKGRCLVSGAGNVAQY 284  
 Db 185 SNQFTSVLTGKLSYGGSLIRPEATGCGVYFAQEMLKDRGRGDFQQRVAISGSGNVAQY 244  
 QY 285 CAELLLKGAIVLSLSDSGYVYEPNGFTREQLOAVQDMKKNSARISEYKSDTAVYVG 344  
 Db 245 AARKVMEMGGKVISLSDSGYVYEPNGFTREQLOAVQDMKKNSARISEYKSDTAVYVG 303  
 QY 345 DRKPWELDCQVDIAPPCATQNEIDEHDAELLIKHGQYVVEGANMPSTNEAIHKYNKAG 404  
 Db 304 EGRRPWGLAC--DIALPCATQNELDAEDARRLLANGCVCVAGANWPSLEAVDLFLEAG 361  
 QY 405 ILYCPGKAANAGGAVVSGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSA-MGPSRRYVNV 463  
 Db 362 ILYAPGKASNAGGAVVSGLEMSQNMRLRWSEGEVDTKLHGIMQSIHHACLLYGBEQGRV 421  
 QY 464 DLAAGANIAGFTKVADAVKAQAV 487  
 Db 422 NYVKGANIAGFVKVADAMLAQGVV 445

## RESULT 14

ADP08330  
 ID ABO71900 standard; protein; 450 AA.

AC ABO71900;

DT 29-JUL-2004 (first entry)

XX Pseudomonas aeruginosa polypeptide #4075.

DE Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.

OS Pseudomonas aeruginosa.

XX US6551795-B1.

PN 22-APR-2003.

PD 18-FEB-1999; 99US-00252991.

PF 18-FEB-1998; 98US-0074788P.

PR 27-JUL-1998; 98US-0094190P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Rubenfield MJ, Nollong J, Deloughery C, Bush D;

XX WPI; 2003-615309/58.

DR N-P8DB; ABD05471.

XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,

PT useful as molecular targets for diagnostics, prophylaxis and treatment of

PT pathological conditions resulting from bacterial infection.

XX Disclosure; SEQ ID NO 20646; 455pp; English.

XX The invention relates to Pseudomonas aeruginosa polypeptides and the  
 CC polynucleotides encoding them. The sequences are useful in diagnosis and  
 CC therapy of pathological conditions, as molecular targets for diagnostics,  
 CC prophylaxis and treatment of pathological conditions resulting from a  
 CC bacterial infection, for evaluating a compound, such as a polypeptide,  
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of  
 CC effective antibacterial targets, as targets for antibacterial drugs,  
 CC including anti-P. aeruginosa drugs, as templates for recombinant  
 CC production of P. aeruginosa-derived peptides or polypeptides, as target  
 CC components for diagnosis and/or treatment of P. aeruginosa-caused  
 CC infection, and in detection of P. aeruginosa sequences or other sequences  
 CC of Pseudomonas species using biochip technology. Sequences ABO67826-

CC ABO484396 represent P. aeruginosa polypeptides of the invention. Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html

XX SQ Sequence 450 AA;

Query Match 52.1%; Score 1309; DB 7; Length 450;

Best Local Similarity 59.2%; Pred. No. 7.9e-116;

Matches 263; Conservative 55; Mismatches 120; Indels 6; Gaps 4;

QY 47 VRQLLTETFMEDPEQOEPMQAVREAVVLSQVPEKRPPELLP--IFKQIPEERVITPVS 104

Db 10 VDAFLERLKRDPDQPEPHQAVEVLRSLWFFLEANPHYLEAGIIRIVEPERAILFRVP 69

QY 105 WLDAGNLQVNRGRVQYSSAIGPYKGLRPHPSVNLIMKFLAPFQIFKNSLTTLPMGG 164

Db 70 WVDQGRVVRNVRGVQMSAIGPYKGLRPHPSVNLGLVKFLAFAEQVFNKSLTTLPMGG 129

QY 165 GKGSDFDPKGSDAEVMRFQSPFMTLQRIHSYVQDVDPAGDVGAREIGYLFQYKRI 224

Db 130 GKGSDFDPKGSDAEVMRFQSPFMTLQRIHSYVQDVDPAGDVGAREIGYLFQYKRI 189

QY 225 TKNYTVLTPKQYGGSEIRPEATGYGAVLVFNVLKDKGSLKGRCLVSGAGNVAQY 284

Db 190 SNQFTSVLTGKLSYGGSLIRPEATGCGVYFAQEMLKDRGRGDFQQRVAISGSGNVAQY 249

QY 285 CAELLLKGAIVLSLSDSGYVYEPNGFTREQLOAVQDMKKNSARISEYKSDTAVYVG 344

Db 250 AARKVMEMGGKVISLSDSGYVYEPNGFTREQLOAVQDMKKNSARISEYKSDTAVYVG 308

QY 345 DRKPWELDCQVDIAPPCATQNEIDEHDAELLIKHGQYVVEGANMPSTNEAIHKYNKAG 404

Db 309 EGRRPWGLAC--DIALPCATQNELDAEDARRLLANGCVCVAGANWPSLEAVDLFLEAG 366

QY 405 ILYCPGKAANAGGAVVSGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSA-MGPSRRYVNV 463

Db 367 ILYAPGKASNAGGAVVSGLEMSQNMRLRWSEGEVDTKLHGIMQSIHHACLLYGBEQGRV 426

QY 464 DLAAGANIAGFTKVADAVKAQAV 487

Db 427 NYVKGANIAGFVKVADAMLAQGVV 450

## RESULT 15

ADP08330

XX ID ADP08330 standard; protein; 444 AA.

AC ADP08330;

XX 26-AUG-2004 (first entry)

XX Neisseria meningitidis MC58 OMV-related membrane protein - SEQ ID 163.

XX outer-membrane vesicle; antibacterial; antiinflammatory;

XX meningococcal protein trafficking; localisation; infection; vaccine;

XX gene therapy.

OS Neisseria meningitidis MC58.

XX WO2004046177-A2.

XX 03-JUN-2004.

XX 17-NOV-2003; 2003WO-IB006281.

XX 15-NOV-2002; 2002GB-00026734.

XX 27-MAR-2003; 2003GB-00007131.

XX (CHIR ) CHIRON SRL.

XX Norais N, Grandi G;

Search completed: September 8, 2005, 02:34:15  
Job time : 97.0793 secs

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OM protein - protein search, using sw model

Run on: September 8, 2005, 02:10:48 ; Search time 95.8047 Seconds  
(without alignments)  
2104.671 Million cell updates/sec

Title: US-10-627-886-4

Perfect score: 2638

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Searched: 1774312 seqs, 393823214 residues

Total number of hits satisfying chosen parameters: 1774312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Query Match | Length | ID | Description          |
|------------|--------|-------------|--------|----|----------------------|
| 1          | 2638   | 100.0       | 512    | 9  | US-09-070-844-4      |
| 2          | 2638   | 100.0       | 512    | 16 | US-10-627-886-4      |
| 3          | 2621   | 99.4        | 526    | 9  | US-09-070-844-2      |
| 4          | 2621   | 99.4        | 526    | 16 | US-10-627-886-2      |
| 5          | 2508   | 95.1        | 487    | 9  | US-09-070-844-24     |
| 6          | 2508   | 95.1        | 487    | 16 | US-10-627-886-24     |
| 7          | 2465   | 93.4        | 476    | 9  | US-09-070-844-26     |
| 8          | 2465   | 93.4        | 476    | 16 | US-10-627-886-26     |
| 9          | 1309   | 49.6        | 444    | 15 | US-10-282-122A-66697 |
| 10         | 1300.5 | 49.3        | 444    | 18 | US-10-988-943-43     |
| 11         | 1297.5 | 49.2        | 444    | 15 | US-10-282-122A-65129 |

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| 12 | 1294.5 | 49.1 | 444 | 15 | US-10-282-122A-66041 |
| 13 | 1294.5 | 49.1 | 444 | 15 | US-10-275-026A-152   |
| 14 | 1287.5 | 48.8 | 449 | 15 | US-10-282-122A-67538 |
| 15 | 1281   | 48.6 | 445 | 15 | US-10-369-493-13947  |
| 16 | 1259   | 47.7 | 454 | 15 | US-10-369-493-9939   |
| 17 | 1257.5 | 47.7 | 462 | 15 | US-10-282-122A-45200 |
| 18 | 1239.5 | 47.0 | 448 | 15 | US-10-282-122A-57310 |
| 19 | 1239.5 | 47.0 | 448 | 18 | US-10-953-901-338    |
| 20 | 1238   | 46.9 | 449 | 14 | US-10-260-877-90     |
| 21 | 1238   | 46.9 | 449 | 15 | US-10-282-122A-58096 |
| 22 | 1230.5 | 46.6 | 449 | 15 | US-10-282-122A-72329 |
| 23 | 1230   | 46.6 | 449 | 15 | US-10-282-122A-66870 |
| 24 | 1214   | 46.0 | 448 | 15 | US-10-282-122A-74024 |
| 25 | 1212   | 45.9 | 448 | 17 | US-10-472-928-2632   |
| 26 | 1211.5 | 45.9 | 448 | 18 | US-10-953-901-340    |
| 27 | 1210.5 | 45.9 | 458 | 15 | US-10-369-493-17284  |
| 28 | 1207.5 | 45.8 | 464 | 15 | US-10-282-122A-51278 |
| 29 | 1205.5 | 45.7 | 424 | 15 | US-10-369-493-617    |
| 30 | 1205.5 | 45.7 | 444 | 15 | US-10-282-122A-48442 |
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| 34 | 1196.5 | 45.4 | 456 | 15 | US-10-425-114-72961  |
| 35 | 1195.5 | 45.3 | 438 | 15 | US-10-369-493-8215   |
| 36 | 1194   | 45.3 | 438 | 15 | US-10-282-122A-60243 |
| 37 | 1191   | 45.1 | 447 | 15 | US-11-073-550-80     |
| 38 | 1191   | 45.1 | 447 | 20 | US-09-738-626-6982   |
| 39 | 1185   | 44.9 | 447 | 9  | US-09-070-844-4      |
| 40 | 1184   | 44.9 | 447 | 20 | US-11-073-550-82     |
| 41 | 1182.5 | 44.8 | 448 | 15 | US-10-282-122A-53998 |
| 42 | 1181   | 44.8 | 447 | 15 | US-10-282-122A-75593 |
| 43 | 1180.5 | 44.7 | 458 | 15 | US-10-282-122A-60810 |
| 44 | 1180   | 44.7 | 447 | 15 | US-10-369-493-295    |
| 45 | 1178   | 44.7 | 447 | 15 | US-10-282-122A-72769 |

ALIGNMENTS

RESULT 1  
US-09-070-844-4  
; Sequence 4, Application US/09070844  
; Patent No. US20020062495A1  
; GENERAL INFORMATION:  
; APPLICANT: Schmidt, Robert R.  
; APPLICANT: Miller, Philip  
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
; TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/09/070,844  
; APPLICATION NUMBER: 08/725,596  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/725,596  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Whitlock, Ted W.  
; REGISTRATION NUMBER: 36,965  
; REFERENCE/DOCKET NUMBER: UF155

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 512 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-070-844-4

Query Match      100.0%; Score 2638; DB 9; Length 512;
Best Local Similarity 100.0%; Pred. No. 2.7e-228;
Matches 512; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOTALVAKPIVACAWRSKRDVRAKAVSLSEQISAMDATTGDTALQKAVQMATKAGT 60
DB 1 MOTALVAKPIVACAWRSKRDVRAKAVSLSEQISAMDATTGDTALQKAVQMATKAGT 60
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DB 61 EGLVHGKINPDVRLTTEIFMKDPQEQEFMQAVREAVSLQVPFVKRPPELLPIFKQIVPEP 120
QY 121 ERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGLRPHPSVNLSTMKFLAPFQIPKN 180
DB 121 ERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGLRPHPSVNLSTMKFLAPFQIPKN 180
QY 181 SLTTLPMGGKGGSDFPDPKGSDAEVMRFQCFMTLQRHISYVQDVDPAGDIGVGARETG 240
DB 181 SLTTLPMGGKGGSDFPDPKGSDAEVMRFQCFMTLQRHISYVQDVDPAGDIGVGARETG 240
QY 241 YLFGQYKRITKNYTGVLTPKGQYGGSEIRPEATGYGAVLFVENVLKDGESLKGKRCILV 300
DB 241 YLFGQYKRITKNYTGVLTPKGQYGGSEIRPEATGYGAVLFVENVLKDGESLKGKRCILV 300
QY 301 SGAGNVAQYCAELLEKGAIVLSLSDSQGYVVEPNPFTREQLQAVQDMKKKNSARISEY 360
DB 301 SGAGNVAQYCAELLEKGAIVLSLSDSQGYVVEPNPFTREQLQAVQDMKKKNSARISEY 360
QY 361 KSDTAVYVGGDRRKPELDCQVDIAFPCCATQNEIDHDAELLIKHGQYVVEGANPSTNE 420
DB 361 KSDTAVYVGGDRRKPELDCQVDIAFPCCATQNEIDHDAELLIKHGQYVVEGANPSTNE 420
QY 421 AIHKYNKAGIIPCPCAAANAGGAVVSGLEMTQNRMSLNWTREVRDKLERIMKDIYDSAM 480
DB 421 AIHKYNKAGIIPCPCAAANAGGAVVSGLEMTQNRMSLNWTREVRDKLERIMKDIYDSAM 480
QY 481 GPSRRYVNDLAAGANIAGFTKVADAVKAQAV 512
DB 481 GPSRRYVNDLAAGANIAGFTKVADAVKAQAV 512
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RESULT 2
US-10-627-886-4
; Sequence 4, Application US/10627886
; Publication No. US20040128710A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; RELATING TO THE -- AND -SUBUNITS OF GLUTAMATE
; DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606-6669
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/627,886
; FILING DATE: 24-Jul-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/070,844
; FILING DATE: 01-MAY-98
; APPLICATION NUMBER: 08/725,596
; FILING DATE: 03-OCT-96
; APPLICATION NUMBER: 08/541,033
; FILING DATE: 06-OCT-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Lloyd, Jeff
; REGISTRATION NUMBER: 35,589
; REFERENCE/DOCKET NUMBER: UP-155CD3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 512 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-627-886-4

Query Match      100.0%; Score 2638; DB 16; Length 512;
Best Local Similarity 100.0%; Pred. No. 2.7e-228;
Matches 512; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOTALVAKPIVACAWRSKRDVRAKAVSLSEQISAMDATTGDTALQKAVQMATKAGT 60
DB 1 MOTALVAKPIVACAWRSKRDVRAKAVSLSEQISAMDATTGDTALQKAVQMATKAGT 60
QY 61 EGLVHGKINPDVRLTTEIFMKDPQEQEFMQAVREAVSLQVPFVKRPPELLPIFKQIVPEP 120
DB 61 EGLVHGKINPDVRLTTEIFMKDPQEQEFMQAVREAVSLQVPFVKRPPELLPIFKQIVPEP 120
QY 121 ERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGLRPHPSVNLSTMKFLAPFQIPKN 180
DB 121 ERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGLRPHPSVNLSTMKFLAPFQIPKN 180
QY 181 SLTTLPMGGKGGSDFPDPKGSDAEVMRFQCFMTLQRHISYVQDVDPAGDIGVGARETG 240
DB 181 SLTTLPMGGKGGSDFPDPKGSDAEVMRFQCFMTLQRHISYVQDVDPAGDIGVGARETG 240
QY 241 YLFGQYKRITKNYTGVLTPKGQYGGSEIRPEATGYGAVLFVENVLKDGESLKGKRCILV 300
DB 241 YLFGQYKRITKNYTGVLTPKGQYGGSEIRPEATGYGAVLFVENVLKDGESLKGKRCILV 300
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DB 301 SGAGNVAQYCAELLEKGAIVLSLSDSQGYVVEPNPFTREQLQAVQDMKKKNSARISEY 360
QY 361 KSDTAVYVGGDRRKPELDCQVDIAFPCCATQNEIDHDAELLIKHGQYVVEGANPSTNE 420
DB 361 KSDTAVYVGGDRRKPELDCQVDIAFPCCATQNEIDHDAELLIKHGQYVVEGANPSTNE 420
QY 421 AIHKYNKAGIIPCPCAAANAGGAVVSGLEMTQNRMSLNWTREVRDKLERIMKDIYDSAM 480
DB 421 AIHKYNKAGIIPCPCAAANAGGAVVSGLEMTQNRMSLNWTREVRDKLERIMKDIYDSAM 480
QY 481 GPSRRYVNDLAAGANIAGFTKVADAVKAQAV 512
DB 481 GPSRRYVNDLAAGANIAGFTKVADAVKAQAV 512
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RESULT 3
US-09-070-844-2
; Sequence 2, Application US/09070844
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; Patent No. US20020062495A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,844
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,596
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UF155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 526 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-070-844-2

Query Match 99.4%; Score 2621; DB 9; Length 526;
Best Local Similarity 97.3%; Pred. No. 9.4e-227;
Matches 512; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 MOTALVAKPIVA-----CAWVRSKRDVRAKAVSLERQISAMDATTGDTFA 46
DB 1 MOTALVAKPIVAAPLAARPCRLAPWPCAWVRSKRDVRAKAVSLERQISAMDATTGDTFA 60
QY 47 LQKAVKQMATKAGTEGLVHGINKPNVDVRLTEIFMKDPEQOEFMQAVREVAVSLQPVFEK 106
DB 61 LQKAVKQMATKAGTEGLVHGINKPNVDVRLTEIFMKDPEQOEFMQAVREVAVSLQPVFEK 120
QY 107 RPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGRFVQYSSAIGPYKGLRFPHSVNL 166
DB 121 RPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGRFVQYSSAIGPYKGLRFPHSVNL 180
QY 167 SIMKFLAFQIFKNSLTTLPMSGGKGSDFDPKGSDAEVMRQCQSFMTLQRHISYVD 226
DB 181 SIMKFLAFQIFKNSLTTLPMSGGKGSDFDPKGSDAEVMRQCQSFMTLQRHISYVD 240
QY 227 VPAGDVGAGAREIGYLFQGYKRTKNTYGVLPKGQYGGSEIRPEATGAGVLFVENVL 286
DB 241 VPAGDVGAGAREIGYLFQGYKRTKNTYGVLPKGQYGGSEIRPEATGAGVLFVENVL 300
QY 287 XDKGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQ 346
DB 301 XDKGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQ 360
QY 347 DMKKKXNSARISYKSDTAVYVGDRLKRWELDCQVDIAFPFCATQNEIDHDAELLKHQC 406
DB 361 DMKKKXNSARISYKSDTAVYVGDRLKRWELDCQVDIAFPFCATQNEIDHDAELLKHQC 420

; Patent No. US20020062495A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/627,886
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/070,844
; FILING DATE: 01-MAY-98
; FILING DATE: 03-OCT-96
; FILING DATE: 06-OCT-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Lloyd, Jeff
; REGISTRATION NUMBER: 35,589
; REFERENCE/DOCKET NUMBER: UF-155CD3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 526 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
; US-10-627-886-2

Query Match 99.4%; Score 2621; DB 16; Length 526;
Best Local Similarity 97.3%; Pred. No. 9.4e-227;
Matches 512; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 MOTALVAKPIVA-----CAWVRSKRDVRAKAVSLERQISAMDATTGDTFA 46
DB 1 MOTALVAKPIVAAPLAARPCRLAPWPCAWVRSKRDVRAKAVSLERQISAMDATTGDTFA 60
QY 47 LQKAVKQMATKAGTEGLVHGINKPNVDVRLTEIFMKDPEQOEFMQAVREVAVSLQPVFEK 106
DB 61 LQKAVKQMATKAGTEGLVHGINKPNVDVRLTEIFMKDPEQOEFMQAVREVAVSLQPVFEK 120
QY 107 RPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGRFVQYSSAIGPYKGLRFPHSVNL 166
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Db 121 REPELLIPKQIVPEPVRITFRVSWLDDAGNLQVNRGFRVQYSALGPYKGLRFPSPVNL 180  
QY 167 SIMKFLAEPQIPKNSLTTLPMGGGKGGSDPDKGSDAEVMRFCQSFMTLQRIHSYVQD 226  
Db 181 SIMKFLAEPQIPKNSLTTLPMGGGKGGSDPDKGSDAEVMRFCQSFMTLQRIHSYVQD 240  
QY 227 VPAGDIGVAREIGYLFQYKRIITKNYTGVLTPKQEGGSGSIRPEATGYGAVLFVENVL 286  
Db 241 VPAGDIGVAREIGYLFQYKRIITKNYTGVLTPKQEGGSGSIRPEATGYGAVLFVENVL 300  
QY 287 KDKGSLKGRCLVSGAGNVAQYCAELLEKGAIVLSLSDSGYVYVPEPNGFTREQLQAVQ 346  
Db 301 KDKGSLKGRCLVSGAGNVAQYCAELLEKGAIVLSLSDSGYVYVPEPNGFTREQLQAVQ 360  
QY 347 DMKKQNGARISEYKSDTAVYVGGDRRKPWELDCQVDIAPPCCATQNEIDHDAELLIKHGC 406  
Db 361 DMKKQNGARISEYKSDTAVYVGGDRRKPWELDCQVDIAPPCCATQNEIDHDAELLIKHGC 420  
QY 407 QYVVEGANPSTNEAIHKYNKAGIICPGKAANAGGAVVSGLEMTQNRMSLNTWTRREVRD 466  
Db 421 QYVVEGANPSTNEAIHKYNKAGIICPGKAANAGGAVVSGLEMTQNRMSLNTWTRREVRD 480  
QY 467 KLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTTKVADAVKAQAV 512  
Db 481 KLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTTKVADAVKAQAV 526

## RESULT 5

US-09-070-844-24  
; Sequence 24, Application US/09070844  
; Patent No. US20020062495A1  
; GENERAL INFORMATION:  
; APPLICANT: Schmidt, Robert R.  
; APPLICANT: Miller, Philip  
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
; TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE  
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/09/070,844  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/725,596  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Whitlock, Ted W.  
; REGISTRATION NUMBER: 36,965  
; REFERENCE/DOCKET NUMBER: UFI155  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (904) 375-8100  
; TELEFAX: (904) 372-5800  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 487 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-070-844-24

Query Match 95.1%; Score 2508; DB 9; Length 487;  
Best Local Similarity 100.0%; Pred. No. 1.3e-216;  
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 27 AVSLEEQISAMDATTTGDFALQKAVKOMATKAGTEGLVHGINKNPDVROLLEIFPMKDPQEQ 86  
Db 2 AVSLEEQISAMDATTTGDFALQKAVKOMATKAGTEGLVHGINKNPDVROLLEIFPMKDPQEQ 61  
QY 87 QEFMQAVREVAVSLQPVFEKRPPELLPIFKQIVPEPVRITFRVSWLDDAGNLQVNRGFRVQ 146  
Db 62 QEFMQAVREVAVSLQPVFEKRPPELLPIFKQIVPEPVRITFRVSWLDDAGNLQVNRGFRVQ 121  
QY 147 YSSAIGPYKGLRFPSPVNL SIMKFLAEPQIPKNSLTTLPMGGGKGGSDPDKGSDAEV 206  
Db 122 YSSAIGPYKGLRFPSPVNL SIMKFLAEPQIPKNSLTTLPMGGGKGGSDPDKGSDAEV 181  
QY 207 MRFQCSFMTLQRIHSYVQDVPAGDIGVAREIGYLFQYKRIITKNYTGVLTPKQEGYGG 266  
Db 182 MRFQCSFMTLQRIHSYVQDVPAGDIGVAREIGYLFQYKRIITKNYTGVLTPKQEGYGG 241  
QY 267 SEIRPEATGYGAVLFVENVLKDGESLKGKCLVSGAGNVAQYCAELLEKGAIVLSLSD 326  
Db 242 SEIRPEATGYGAVLFVENVLKDGESLKGKCLVSGAGNVAQYCAELLEKGAIVLSLSD 301  
QY 327 SOGYVYVPEPNGFTREQLQAVQDMKKQNGARISEYKSDTAVYVGGDRRKPWELDCQVDIAPP 386  
Db 302 SOGYVYVPEPNGFTREQLQAVQDMKKQNGARISEYKSDTAVYVGGDRRKPWELDCQVDIAPP 361  
QY 387 CATQNEIDHDAELLIKHGCQYVVEGANPSTNEAIHKYNKAGIICPGKAANAGGAVV 446  
Db 362 CATQNEIDHDAELLIKHGCQYVVEGANPSTNEAIHKYNKAGIICPGKAANAGGAVV 421  
QY 447 GLEMTQNRMSLNTWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTTKVADAV 506  
Db 422 GLEMTQNRMSLNTWTRREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTTKVADAV 481  
QY 507 KAQAV 512  
Db 482 KAQAV 487

## RESULT 6

US-10-627-886-24  
; Sequence 24, Application US/10627886  
; Publication No. US20040128710A1  
; GENERAL INFORMATION:  
; APPLICANT: Schmidt, Robert R.  
; APPLICANT: Miller, Philip  
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
; RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE  
; DEHYDROGENASES AND METHODS OF USE  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606-6669  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/627,886  
; FILING DATE: 24-Jul-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/070,844  
; FILING DATE: 01-MAY-98  
; APPLICATION NUMBER: 08/725,596  
; FILING DATE: 03-OCT-96

APPLICATION NUMBER: 08/541,033  
FILING DATE: 06-OCT-95  
ATTORNEY/AGENT INFORMATION:  
NAME: Lloyd, Jeff  
REGISTRATION NUMBER: 35,589  
REFERENCE/DOCKET NUMBER: UF-155CD3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (352) 375-8100  
TELEFAX: (352) 372-5800  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 487 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 24:  
US-10-627-886-24

Query Match 95.1%; Score 2508; DB 16; Length 487;  
Best Local Similarity 100.0%; Pred. No. 1.3e-216;  
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 AVSLEBQISAMDATGDTALQKAVKQMATKAGTEGLVHGINKNPDVROLLEIFMKDPEQ 86  
DB 2 AVSLEBQISAMDATGDTALQKAVKQMATKAGTEGLVHGINKNPDVROLLEIFMKDPEQ 61  
QY 87 QEFMQAVREAVSLQPVFEKPELLPIFKQIVPEPVTFRVSWLDDAGNLQVNRGFRVQ 146  
DB 62 QEFMQAVREAVSLQPVFEKPELLPIFKQIVPEPVTFRVSWLDDAGNLQVNRGFRVQ 121  
QY 147 YSSAIGPYKGLRFPSPVNLKFLAPQIFKNSLTTLPMGGGKGGSDFPKGSDAEV 206  
DB 122 YSSAIGPYKGLRFPSPVNLKFLAPQIFKNSLTTLPMGGGKGGSDFPKGSDAEV 181  
QY 207 MFPCOSFTELORHISYQDVDPAGDIGVAREIGVLFQYKRITKNYTGVLTPKQEGYCG 266  
DB 182 MFPCOSFTELORHISYQDVDPAGDIGVAREIGVLFQYKRITKNYTGVLTPKQEGYCG 241  
QY 267 SEIRPEATGYGAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLEKGAI VLSLSD 326  
DB 242 SEIRPEATGYGAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLEKGAI VLSLSD 301  
QY 327 SQGYVPEPGFTREQLQAVQDMKKKNSARISEYKSDTAVYVGGDRRKPELDCQVDIAPP 386  
DB 302 SQGYVPEPGFTREQLQAVQDMKKKNSARISEYKSDTAVYVGGDRRKPELDCQVDIAPP 361  
QY 387 CATONEIDHDAELLKHGCGQYVVEGANMPSTNEAIHKYNKAGI IYCPGKAANAGGVAVS 446  
DB 362 CATONEIDHDAELLKHGCGQYVVEGANMPSTNEAIHKYNKAGI IYCPGKAANAGGVAVS 421  
QY 447 GLEMTQNRMSLNTREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTTKVADAV 506  
DB 422 GLEMTQNRMSLNTREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTTKVADAV 481  
QY 507 KAQGVAV 512  
DB 482 KAQGVAV 487

RESULT 7  
US-09-070-844-26  
; Sequence 26, Application US/09070844  
; Patent No. US20020062495A1  
; GENERAL INFORMATION:  
; APPLICANT: Schmidt, Robert R.  
; APPLICANT: Miller, Philip  
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
; TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE  
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/070,844  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/725,596  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Whitlock, Ted W.  
REGISTRATION NUMBER: 36,965  
REFERENCE/DOCKET NUMBER: UF155  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 476 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-070-844-26

Query Match 93.4%; Score 2465; DB 9; Length 476;  
Best Local Similarity 100.0%; Pred. No. 9e-213;  
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 MDATTGDTALQKAVKQMATKAGTEGLVHGINKNPDVROLLEIFMKDPEQBFMQAVREV 96  
DB 1 MDATTGDTALQKAVKQMATKAGTEGLVHGINKNPDVROLLEIFMKDPEQBFMQAVREV 60  
QY 97 AVSLQPVFEKPELLPIFKQIVPEPVTFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 156  
DB 61 AVSLQPVFEKPELLPIFKQIVPEPVTFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120  
QY 157 GLRHPSPVNLKFLAPQIFKNSLTTLPMGGGKGGSDFPKGSDAEVNRFCSFMTE 216  
DB 121 GLRHPSPVNLKFLAPQIFKNSLTTLPMGGGKGGSDFPKGSDAEVNRFCSFMTE 180  
QY 217 LQRHISYQDVDPAGDIGVAREIGVLFQYKRITKNYTGVLTPKQEGYGGSEIRPEATGY 276  
DB 181 LQRHISYQDVDPAGDIGVAREIGVLFQYKRITKNYTGVLTPKQEGYGGSEIRPEATGY 240  
QY 277 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLEKGAI VLSLSDSQGYVPENG 336  
DB 241 GAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLEKGAI VLSLSDSQGYVPENG 300  
QY 337 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGGDRRKPELDCQVDIAPPATONEIDEH 396  
DB 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGGDRRKPELDCQVDIAPPATONEIDEH 360  
QY 397 DAELLKHGCGQYVVEGANMPSTNEAIHKYNKAGI IYCPGKAANAGGVAVSGLMTQNRMS 456  
DB 361 DAELLKHGCGQYVVEGANMPSTNEAIHKYNKAGI IYCPGKAANAGGVAVSGLMTQNRMS 420  
QY 457 LNTREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTTKVADAVKAQGVAV 512  
DB 421 LNTREVRDKLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTTKVADAVKAQGVAV 476

RESULT 8  
US-10-627-886-26  
; Sequence 26, Application US/10627886  
; Publication No. US20040128710A1  
; GENERAL INFORMATION:



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125 GKGSDFDPKGSDAEWMRFQCSFMSELYRHHVGADLDVPAGDVGAREBIGYLFQGYKRL 184
Qy 250 TKNYTVGLVTPKQEQYGGSEIRPEATGYGAVLFEVENVLKDGBESLKGKRLVSGAGNVAQY 309
Db 185 SNQFTSVLTGKGLSYGGSLIRPEATGFCGYPAQEMLKDRGRGFDGQRFVAISGSGNVAQY 244
Qy 310 CAEILLEKGAIVLSLSDSQGYVYEPNGFTREOLQAVODMKKNNSARISEYKSDTAVYVG 369
Db 245 AARKVMWGGKVISLSDSEGLIYAEAGLSDEQWEYLMELKNVRR-GRIREMAEQFSLOPL 303
Qy 370 DRRKPWELDCQVDIAFPQCATQNEIDEHDAELLIKHGQCYVVEGANMPSTNEAIHKYNKAG 429
Db 304 EGRRPWGLAC--DIALPCATQNELDAEDARRLLANGCVCVAEGANMPSTLEAVDLFLEAG 361
Qy 430 ILYCPGKAANAGGVAVSGLEMTQNRMSLNWTFEYRDKLERIMKDIYDQA-MGPSRRYNY 488
Db 362 ILYAPGKASNAGGVAVSGLEMSQNAURLRWSEGEVDTKLHLGIMQSIHHACLLYGBEQGRV 421
Qy 489 DLAAAGANIAGFTKVADAVKAQAV 512
Db 422 NYVKGANIAGFKVADAMLAQGCV 445

RESULT 10
US-10-988-943-43
; Sequence 43, Application US/10988943
; Publication No. US20050176085A1
; GENERAL INFORMATION:
; APPLICANT: Center for Genetic Engineering and Biotechnology
; TITLE OF INVENTION: METHOD OF SELECTIVE PEPTIDE ISOLATION FOR THE
; TITLE OF INVENTION: IDENTIFICATION AND QUANTITATIVE ANALYSIS OF PROTEINS IN
; TITLE OF INVENTION: COMPLEX MIXTURES.
; FILE REFERENCE: Proteomics CU2003-269
; CURRENT APPLICATION NUMBER: US/10/988,943
; CURRENT FILING DATE: 2004-11-15
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Neisseria meningitidis (group B)
US-10-988-943-43

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|                       |       |  |                |            |
|-----------------------|-------|--|----------------|------------|
| Query Match           | 49.3% | Score 1300.5   | DB 18          | Length 444 |
| Best Local Similarity | 57.4% | Pred. No. 5.8e-108   |                |            |
| Matches               | 257   | Conservative 72  | Mismatches 104 | Indels 15  |
| Gaps                  |       |  |                |            |
| Qy                    | 71    | DVRQLLTETIFMKDPEQEFQMAQREVAVSLQVPFVKRPPELL--PFPKQIVPBPVITPRV   | 128            |            |
| Db                    | 3     | DLNTLTFANLKNRPNQEPFHQAEEVFMFSLDPFLAKNPKYTQQSLLRIVERPVMFVRV     | 62             |            |
| Qy                    | 129   | SWLDDAGNLQVNRGRVVOYSSAIGPYKGLGRPHSPVNLISIMKFLAFEQIFKNLSLTLLPVG | 188            |            |
| Db                    | 63    | TWQDDKGVQVNRGRVVOYSSAIGPYKGLGRPHFPVDLGVLLKFLAFEPQVFNKALTTLLPVG | 122            |            |
| Qy                    | 189   | GKGGSDFDPKGSDAEYVMRFQSPMTLQORHISYVQDVPAGDIGVGAREIGYLFQGYKR     | 248            |            |
| Db                    | 123   | GKGGSDFDPKGSDAEYVMRFQAPMTLEYRHHGADTDPAGDIGVGGREIGYLFQGYKK      | 182            |            |
| Qy                    | 249   | ITKNYTGVLTPKQBGYGGSEIRPEATGCAVLFEVNLKDKGESLKGRCILVSGAGNVAQ     | 308            |            |
| Db                    | 183   | IRNEFSSVLTGKLEWGGSLIRPEATGTGCVYFAQMLQTRNDSPGGRKRVITSGSGNVAQ    | 242            |            |
| Qy                    | 309   | YCAELLLEKGAIVLSLSDSQGVYVEP-NGFTREQLQAVODMKKKNNSARISEYKSDTAVY   | 367            |            |
| Db                    | 243   | YAAEKAQLQGAHVITVSDNSGFLVPDDEGMTAQALALIELKEVRRE-RVATYAKEGQLQ    | 301            |            |
| Qy                    | 368   | VGDRRKWELDCQVDIAPPCATQNEIDSHDAELITKHGQYVVEGANMPSNTEAITHKNK     | 427            |            |
| Db                    | 302   | YFEKQKPGV--AAEIALPCATQNELDEEAKTLLANGCYVVAEGANMPSILGAVEQFIK     | 359            |            |
| Qy                    | 428   | AGLIYCPGAANAGGVAVSGLEMTQNRMSLNWTRREVRDKLERIMKDIYDSAMGSPRY-     | 486            |            |

```

Db      360 AGILYAPGKASNAGVATSGLEMSQNAIRLSWTREEDVQDRLFGIMQSIHESCL-----KYG 415
Qy      487  ---NVDLAAGANIAGFTKVADAVKAQG 510
          |: ||||| |||||: |||
Db      416 KVGDTVMVYNGANIAGFKVADAMLAQG 443

RESULT 11
US-10-282-122A-65129
; Sequence 65129, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282.122A

```

```

CORRENT FILING DATE: 2003-02-20
PRIORITY APPLICATION NUMBER: 60/191,078
PRIORITY FILING DATE: 2000-03-21
PRIORITY APPLICATION NUMBER: 60/206,848
PRIORITY FILING DATE: 2000-05-23
PRIORITY APPLICATION NUMBER: 60/207,727
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: 60/230,335
PRIORITY FILING DATE: 2000-09-06
PRIORITY APPLICATION NUMBER: 60/230,347
PRIORITY FILING DATE: 2000-09-09
PRIORITY APPLICATION NUMBER: 60/242,578
PRIORITY FILING DATE: 2000-10-23
PRIORITY APPLICATION NUMBER: 60/253,625
PRIORITY FILING DATE: 2000-11-27
PRIORITY APPLICATION NUMBER: 60/257,931
PRIORITY FILING DATE: 2000-12-22
PRIORITY APPLICATION NUMBER: 60/267,636
PRIORITY FILING DATE: 2001-02-09
PRIORITY APPLICATION NUMBER: 60/269,308
PRIORITY FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 65129
LENGTH: 444
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-282-122A-65129

```

|    | Query Match           | 49.2%  | Score 1297.5       | DB 15          | Length 444 |
|----|-----------------------|--|--------------------|----------------|------------|
|    | Best Local Similarity | 57.4%  | Pred. No. 1.1e-107 |                |            |
|    | Matches 257           | Conservative   | 70                 | Mismatches 106 | Indels 15  |
|    |                       |  |                    |                | Gaps 6     |
| Qy | 71                    | DVRQLLTETIFMKDPEQQEWFMOAAREVAVSLQPVFEKRPELL--PIFKQIVQPERVITR | 128                |                |            |
| Db | 3                     | DLNLTFLANLQKRPNQBPFFHQAEVEVFWMSLDFFLAKNPKYTQQSLERIVQPERVVMR  | 62                 |                |            |
| Qy | 129                   | SWLDDAGNLQVNRGRFYQVYSSAIGPYKGGRLRPHSPVNLISIMKFLAFEQIFKNSLTTL | 188                |                |            |
| Db | 63                    | TWQDDRGQVQVNRGRYQMSAIGPYKGGRLRFHFTVDLGVLFKLAFAQVFNALTTLP     | 122                |                |            |
| Qy | 189                   | GGKGGSDFDPKGKSDAENVPRCSQFWTLEQRHISVYQDVPAGDTGVGARETGYLFGQYKR | 248                |                |            |
| Db | 123                   | GGKGGSDFDPKGKSDAENVPRFQCAFMTLRYHIGADTDPAGDITGVGARETGYLFGQYKK | 182                |                |            |



| Matches | 259; Conservative | 55; Mismatches       | 124; Indels          | 7; Gaps                | 4;              |
|---------|-------------------|----------------------|----------------------|------------------------|-----------------|
| Qy      | 72                | VROLLTEIFMKDPEQBFMOA | REVAVSLOPVFKRPELLP-- | IFKQIVBPERVITFRVS      | 129             |
| Db      | 8                 | VDNFLARLKQDPQCPQEFHO | AVBEVLRTLPFLEANPHYLQ | SGSLTFRMVEPERAVLFRVS   | 67              |
| Qy      | 130               | WLDDAGNLQVNRFRVGYSSA | IPYKGGLRPHSPVNL      | IMKFLAFEOIFKNSLTTLPMGG | 189             |
| Db      | 68                | WVDDQGVQVNRGYRIOMSS  | RAIPYKGGLRPHSPVNL    | SVLKFLEQVFKNSLTSLPMGG  | 127             |
| Qy      | 190               | KGKGSDFDPKGGKSDAEV   | RRFCQSFMTLQRHISYQ    | VDVPAGDIGVGAREIGYLFQ   | YKRI 249        |
| Db      | 128               | KGKGSDFDPKGGKSDAEV   | RRFCQSFMTLQRHIGAD    | CDVPAGDIGVGAREIGFMFQ   | YKRL 187        |
| Qy      | 250               | TKNYTVGLTPKGOBYGSG   | SEIRPATGVAVLFVENV    | LKDKGESLKGKRCCLVSGAG   | NAOY 309        |
| Db      | 188               | ANOFTSVLTGKGMTYGSG   | LLIRPATGVGYFAEEM     | LKQDKRIDGRVAVVSGSG     | NAOY 247        |
| Qy      | 310               | CABELLKGAIVLSLSDS    | QSGYVYPNGFTREQ       | LQAVQDMKKONNSARISEY    | KSOTAVYVG 369   |
| Db      | 248               | AARKVMDLGGKVISLSD    | SEGLTYAEAGLTDQ       | WDALMELKNVXR-GRIS      | ELAGQFGLFGR 306 |
| Qy      | 370               | DRKPKWELDCQVDIAP     | PCATONEIDEHDAELL     | LKHGCOYVVEGANMSTNE     | AIHKYNKAG 429   |
| Db      | 307               | KGQTPWSLPC--DIALP    | CATONELGAEADART      | LRLNGCICVAEGANMPTT     | LEAVDIFLDAG 364 |
| Qy      | 430               | IICPGKAANAGGVAVSG    | LEBMTONRSLNWTRE      | VRDKLERIMKDIDYDSAM-    | -GPSRRYN 487    |
| Db      | 365               | ILYAPKASNAGGVAVSG    | LEMSQVNRMLLTAGE      | VDSKLNNIMQSIHACV       | HYGEEADGR 424   |
| Qy      | 488               | VDLAAGANTAGTKVAD     | AVKAQGA              | V 512                  |                 |
| Db      | 425               | INVYKGANITAGFKV      | ADAMLAQGV            | V 449                  |                 |

```

US-10-282-122A-67538
: Sequence 67538, Application US/10282122A
: Publication No. US20040029129A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Liangsu
: APPLICANT: Zamudio, Carlos
: APPLICANT: Malone, Cheryl
: APPLICANT: Haselbeck, Robert
: APPLICANT: Ohlsen, Kari
: APPLICANT: Zyskind, Judith
: APPLICANT: Wall, Daniel
: APPLICANT: Trawick, John
: APPLICANT: Carr, Grant
: APPLICANT: Yamamoto, Robert
: APPLICANT: Forsyth, R.
: APPLICANT: Xu, H.
: TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
: FILE REFERENCE: ELITRA.034A

```

|    |                           |            |
|----|---------------------------|------------|
| 1  | CURRENT FILING DATE:      | 2003-02-20 |
| 2  | PRIOR APPLICATION NUMBER: | 60/191,078 |
| 3  | PRIOR FILING DATE:        | 2000-03-21 |
| 4  | PRIOR APPLICATION NUMBER: | 60/206,848 |
| 5  | PRIOR FILING DATE:        | 2000-05-23 |
| 6  | PRIOR APPLICATION NUMBER: | 60/207,727 |
| 7  | PRIOR FILING DATE:        | 2000-05-26 |
| 8  | PRIOR APPLICATION NUMBER: | 60/230,335 |
| 9  | PRIOR FILING DATE:        | 2000-09-06 |
| 10 | PRIOR APPLICATION NUMBER: | 60/230,347 |
| 11 | PRIOR FILING DATE:        | 2000-09-09 |
| 12 | PRIOR APPLICATION NUMBER: | 60/242,578 |
| 13 | PRIOR FILING DATE:        | 2000-10-23 |
| 14 | PRIOR APPLICATION NUMBER: | 60/253,625 |
| 15 | PRIOR FILING DATE:        | 2000-11-27 |
| 16 | PRIOR APPLICATION NUMBER: | 60/257,931 |
| 17 | PRIOR FILING DATE:        | 2000-12-22 |
| 18 | PRIOR APPLICATION NUMBER: | 60/267,636 |
| 19 | PRIOR FILING DATE:        | 2001-02-09 |
| 20 | PRIOR APPLICATION NUMBER: | 60/269,308 |

; NUMBER OF SEQ ID NOS: 78614

```

; SEQ ID NO 67538
; I-ENCTH: 448

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ORGANISM: *Pseudomonas putida*

Db 125 GKGSDFDPKGSDAEVMRFCQAFMSELYRHHIGADVDPAGDIGVGAREIGFLFGQYKRL 184  
QY 250 TQNYTCVLTPKQOEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKCLVSGAGNVAQY 309  
Db 185 SNQFTSVLTGKGMTYGGSLIRPEATGFCGCVFAEEMLKRRREQVEGKRVAISGSGNVAQY 244  
QY 310 CAELLEKGAIVLSLSDSQGVYVEPENGPTREQLQAVQDMKKKNSARISEYKSDTAVVVG 369  
Db 245 AARKVMDLGGKVISLSDSEGTLYCEAGLSEEQWLALLELKNVKR-GRISELASAFGLEFR 303  
QY 370 DRKPKWELDCQVDIAPPQATONEIDEHDAELLIKHCQYVVEGAMNPSTNEAIHKYNKAG 429  
Db 304 AGQLFWSLPC--DIALPCATQNELDAESARTLLRNGCVCVAEGANWPTTLEAVDIFIEAG 361  
QY 430 IYCFGKAANAGGAVSGLEMTQNMSLNWTREEVYRDKLERIMKDIYDSAMG-PSRRYNV 488  
Db 362 ILFAPGKASNAGGAVSGLEMSQNAWRLMTGGEVDSKLHGIMQSIHHACVHYGENGRI 421  
QY 489 DLAAGANIAGFTKVADAVKAQAV 512  
Db 422 NYVKGANIAGFVKVADAMLAQGVV 445

Search completed: September 8, 2005, 02:38:54  
Job time : 97.8047 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 8, 2005, 02:01:27 ; Search time 27.4224 Seconds  
(without alignments)  
1393.764 Million cell updates/sec

Title: US-10-627-886-4  
Perfect score: 2638  
Sequence: 1 MOTALVAKPIVACAWRSRAK.....GANIAGFTKVDVAKQAGAV 512

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/1aa/5A-COMB.pep:\*  
2: /cgn2\_6/prodata/1/1aa/5B-COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/6A-COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/6B-COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/PCTUS-COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | ID | Description          |
|------------|--------|-------------|--------|----|----------------------|
| 1          | 2638   | 100.0       | 512    | 2  | US-08-541-033A-4     |
| 2          | 2638   | 100.0       | 512    | 2  | US-08-828-451-4      |
| 3          | 2621   | 99.4        | 526    | 2  | US-08-541-033A-2     |
| 4          | 2621   | 99.4        | 526    | 2  | US-08-828-451-2      |
| 5          | 2508   | 95.1        | 487    | 2  | US-08-541-033A-24    |
| 6          | 2508   | 95.1        | 487    | 2  | US-08-828-451-24     |
| 7          | 2465   | 93.4        | 476    | 2  | US-08-541-033A-26    |
| 8          | 2465   | 93.4        | 476    | 2  | US-08-828-451-26     |
| 9          | 1309   | 49.6        | 450    | 4  | US-09-252-991A-20646 |
| 10         | 1257.5 | 47.7        | 467    | 4  | US-09-328-352-5725   |
| 11         | 1234.5 | 46.8        | 448    | 4  | US-09-134-000C-3884  |
| 12         | 1221   | 46.3        | 448    | 4  | US-09-583-110-4489   |
| 13         | 1201   | 45.5        | 447    | 2  | US-08-886-640-3      |
| 14         | 1201   | 45.5        | 447    | 3  | US-08-884-235-11     |
| 15         | 1200   | 45.5        | 447    | 1  | US-08-370-193A-11    |
| 16         | 1191   | 45.1        | 452    | 4  | US-09-489-039A-7937  |
| 17         | 1177.5 | 44.6        | 446    | 4  | US-09-543-681A-6657  |
| 18         | 1177   | 44.6        | 447    | 3  | US-08-508-761B-6     |
| 19         | 1147   | 43.5        | 461    | 3  | US-09-171-337A-5     |
| 20         | 1147   | 43.5        | 461    | 4  | US-09-631-022-5      |
| 21         | 1143   | 43.3        | 449    | 1  | US-08-831-753-1      |
| 22         | 1037.5 | 39.3        | 454    | 4  | US-09-538-092-767    |
| 23         | 1012   | 38.4        | 368    | 4  | US-09-107-433-4041   |
| 24         | 788.5  | 29.9        | 298    | 4  | US-09-248-796A-17483 |
| 25         | 552.5  | 20.9        | 420    | 3  | US-09-134-001C-3103  |
| 26         | 537.5  | 20.4        | 374    | 4  | US-09-710-279-2162   |
| 27         | 537    | 20.4        | 509    | 4  | US-09-902-540-11352  |

|    |       |      |      |   |                      |                   |
|----|-------|------|------|---|----------------------|-------------------|
| 28 | 519   | 19.7 | 420  | 3 | US-09-239-303-9      | Sequence 9, Appli |
| 29 | 482.5 | 18.3 | 409  | 4 | US-09-902-540-12638  | Sequence 12638, A |
| 30 | 476.5 | 18.1 | 421  | 3 | US-09-239-303-2      | Sequence 2, Appli |
| 31 | 458.5 | 17.4 | 427  | 4 | US-09-328-352-6130   | Sequence 6130, Ap |
| 32 | 441   | 16.7 | 432  | 4 | US-09-489-039A-13935 | Sequence 13935, A |
| 33 | 385   | 14.6 | 87   | 2 | US-08-461-990B-22    | Sequence 22, Appl |
| 34 | 368   | 13.9 | 87   | 2 | US-08-461-990B-20    | Sequence 20, Appl |
| 35 | 364.5 | 13.8 | 558  | 4 | US-09-538-092-1153   | Sequence 1153, Ap |
| 36 | 357   | 13.5 | 87   | 2 | US-08-461-990B-23    | Sequence 23, Appl |
| 37 | 357   | 13.5 | 558  | 4 | US-09-538-092-832    | Sequence 832, App |
| 38 | 357   | 13.5 | 575  | 4 | US-09-949-016-7622   | Sequence 7622, Ap |
| 39 | 357   | 13.5 | 575  | 4 | US-09-949-016-7623   | Sequence 7623, Ap |
| 40 | 346   | 13.1 | 176  | 4 | US-09-248-796A-17482 | Sequence 17482, A |
| 41 | 168   | 6.4  | 87   | 2 | US-08-461-990B-21    | Sequence 21, Appl |
| 42 | 157.5 | 6.0  | 366  | 2 | US-08-804-699-2      | Sequence 2, Appli |
| 43 | 139.5 | 5.3  | 356  | 2 | US-08-461-990B-122   | Sequence 2, Appli |
| 44 | 138   | 5.2  | 1092 | 4 | US-09-538-092-122    | Sequence 122, App |
| 45 | 131   | 5.0  | 351  | 4 | US-09-198-452A-991   | Sequence 991, App |

## ALIGNMENTS

RESULT 1  
US-08-541-033A-4  
; Sequence 4, Application US/08541033A  
; Patent No. 5879941  
; GENERAL INFORMATION:  
; APPLICANT: Schmidt, Robert R.  
; APPLICANT: Miller, Philip  
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
; TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE  
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/541.033A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Whitlock, Ted W.  
; REGISTRATION NUMBER: 36,965  
; REFERENCE/DOCKET NUMBER: UF155  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (904) 375-8100  
; TELEFAX: (904) 372-5800  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 512 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-541-033A-4

Query Match 100.0%; Score 2638; DB 2; Length 512;  
Best Local Similarity 100.0%; Pred. No. 5.7e-235;  
Matches 512; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MOTALVAKPIVACAWRSRAKDVRAKAVLSLEQISAMDATTGDTFALQKAVKQMATKAGT 60  
DB 1 MOTALVAKPIVACAWRSRAKDVRAKAVLSLEQISAMDATTGDTFALQKAVKQMATKAGT 60

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Db 121 ERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGGRLRPHPSVNLIMKFLAFQIIPKN 180
QY 181 SLTTLPMGGGKGGSDFDPKGSDAEVMRFCQSPMTLQRHISYVQDVPAGDIGVGAREIG 240
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Db 301 SGAGNVAQYCAELLEKGAIVLSLSDSQYVYEPNGFTREQLQAVQDMKKKNNNSARISEY 360
QY 361 KSDTAVYVGDRLKPELDCQVDIAPPCATQNEIDEHDAELLIKHGCGQYVVEGANMPSTNE 420
Db 361 KSDTAVYVGDRLKPELDCQVDIAPPCATQNEIDEHDAELLIKHGCGQYVVEGANMPSTNE 420
QY 421 AIHKYNKAGIICPGKAANAGGAVVSGLEMTQNRMSLNTWTRREVRDKLERIMKOIYDSAM 480
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QY 481 GPSRRYVNDLAAGANIAGFTKVVADAVKAQGA 512
Db 481 GPSRRYVNDLAAGANIAGFTKVVADAVKAQGA 512
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## RESULT 2

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US-08-828-451-4
; Sequence 4, Application US/08828451
; Patent No. 5985634
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESS: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,451
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,033
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UFI155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 512 amino acids
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-828-451-4
Query Match 100.0%; Score 2638; DB 2; Length 512;
Best Local Similarity 100.0%; Pred. No. 5.7e-235; Indels 0; Gaps 0;
Matches 512; Conservative 0; Mismatches 0;
QY 1 MOTALVAKPIVACAWRSKRDVRAKAVSLSEEQISAMDATTTGDTALQKAVKQMATKAGT 60
Db 1 MOTALVAKPIVACAWRSKRDVRAKAVSLSEEQISAMDATTTGDTALQKAVKQMATKAGT 60
QY 61 EGLVHGIIKNDVRLQLTEIFMKDPEQDFMQAVREAVSLQVPEKRPPELLPIPKQIYEP 120
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Db 181 SLTTLPMGGGKGGSDFDPKGSDAEVMRFCQSPMTLQRHISYVQDVPAGDIGVGAREIG 240
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Db 241 YLFGQYKRITKNTYTGVLTPKQGEYGGSEIRPEATGYGAVLFVENVLKDKGSLKGRCLV 300
QY 301 SGAGNVAQYCAELLEKGAIVLSLSDSQYVYEPNGFTREQLQAVQDMKKKNNNSARISEY 360
Db 301 SGAGNVAQYCAELLEKGAIVLSLSDSQYVYEPNGFTREQLQAVQDMKKKNNNSARISEY 360
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Db 361 KSDTAVYVGDRLKPELDCQVDIAPPCATQNEIDEHDAELLIKHGCGQYVVEGANMPSTNE 420
QY 421 AIHKYNKAGIICPGKAANAGGAVVSGLEMTQNRMSLNTWTRREVRDKLERIMKOIYDSAM 480
Db 421 AIHKYNKAGIICPGKAANAGGAVVSGLEMTQNRMSLNTWTRREVRDKLERIMKOIYDSAM 480
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Db 481 GPSRRYVNDLAAGANIAGFTKVVADAVKAQGA 512
RESULT 3
US-08-541-033A-2
; Sequence 2, Application US/08541033A
; Patent No. 5879941
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESS: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,033A
; FILING DATE:
; CLASSIFICATION: 435
```

ATTORNEY/AGENT INFORMATION:  
NAME: Whitlock, Ted W.  
REGISTRATION NUMBER: 36,965  
REFERENCE/DOCKET NUMBER: UF155  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 526 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-541-033A-2

Query Match 99.4%; Score 2621; DB 2; Length 526;  
Best Local Similarity 97.3%; Pred. No. 2.2e-233;  
Matches 512; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 MOTALVAKPIVA-----CAWVRSKRDVRAKAVSLEEQISAMDATTCGDTFA 46  
Db 1 MOTALVAKPIVAAPLAARPRCLAPWPCAWVRSKRDVRAKAVSLEEQISAMDATTCGDTFA 60

QY 47 LQKAVKQMATKAGTEGLVHGIKNPVRLTTEIFMKDPEQEFMQAVREVAVSLQPVFEK 106  
Db 61 LQKAVKQMATKAGTEGLVHGIKNPVRLTTEIFMKDPEQEFMQAVREVAVSLQPVFEK 120

QY 107 RPELLPIFKQIVPEPVRITFRVSWLDDAGNLQVNRGRFRVQYSSAIGPYKGLRFHPSVNL 166  
Db 121 RPELLPIFKQIVPEPVRITFRVSWLDDAGNLQVNRGRFRVQYSSAIGPYKGLRFHPSVNL 180

QY 167 SIMKFLAFAQIFKNSLTTLPMGGGKGGSDPDPKGSDAEVMRFCSQFMTLQRHISYVQD 226  
Db 181 SIMKFLAFAQIFKNSLTTLPMGGGKGGSDPDPKGSDAEVMRFCSQFMTLQRHISYVQD 240

QY 227 VPAGDIGVGAREIGYLFQYKRITKNYTGVLTPKQEGYGGSEIRPEATGYGAVLFVENVL 286  
Db 241 VPAGDIGVGAREIGYLFQYKRITKNYTGVLTPKQEGYGGSEIRPEATGYGAVLFVENVL 300

QY 287 KDKGSLKGKRCCLVSGAGNVAQYCAELLEKGAI VLSLSDSQYVYEPNGFTREQLQAVQ 346  
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Db 361 DMKKKNSARISYKSDTAVYVGDRLKPELDCQVDIAFPFCATQNEIDHDAELLIKHGC 420

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Db 421 QYVVEGANPSTNEAIIHKYNKAGIICPGKAANAGGAVVSGLEMTQNRMSLNWTRREVRD 480

QY 467 KLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQAV 512  
Db 481 KLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQAV 526

RESULT 4  
US-08-828-451-2  
Sequence 2, Application US/08828451  
Patent No. 5985634  
GENERAL INFORMATION:  
APPLICANT: Schmidt, Robert R.  
APPLICANT: Miller, Philip  
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE  
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA

ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/828,451  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/541,033  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Whitlock, Ted W.  
REGISTRATION NUMBER: 36,965  
REFERENCE/DOCKET NUMBER: UF155  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 526 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-828-451-2

Query Match 99.4%; Score 2621; DB 2; Length 526;  
Best Local Similarity 97.3%; Pred. No. 2.2e-233;  
Matches 512; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 MOTALVAKPIVA-----CAWVRSKRDVRAKAVSLEEQISAMDATTCGDTFA 46  
Db 1 MOTALVAKPIVAAPLAARPRCLAPWPCAWVRSKRDVRAKAVSLEEQISAMDATTCGDTFA 60

QY 47 LQKAVKQMATKAGTEGLVHGIKNPVRLTTEIFMKDPEQEFMQAVREVAVSLQPVFEK 106  
Db 61 LQKAVKQMATKAGTEGLVHGIKNPVRLTTEIFMKDPEQEFMQAVREVAVSLQPVFEK 120

QY 107 RPELLPIFKQIVPEPVRITFRVSWLDDAGNLQVNRGRFRVQYSSAIGPYKGLRFHPSVNL 166  
Db 121 RPELLPIFKQIVPEPVRITFRVSWLDDAGNLQVNRGRFRVQYSSAIGPYKGLRFHPSVNL 180

QY 167 SIMKFLAFAQIFKNSLTTLPMGGGKGGSDPDPKGSDAEVMRFCSQFMTLQRHISYVQD 226  
Db 181 SIMKFLAFAQIFKNSLTTLPMGGGKGGSDPDPKGSDAEVMRFCSQFMTLQRHISYVQD 240

QY 227 VPAGDIGVGAREIGYLFQYKRITKNYTGVLTPKQEGYGGSEIRPEATGYGAVLFVENVL 286  
Db 241 VPAGDIGVGAREIGYLFQYKRITKNYTGVLTPKQEGYGGSEIRPEATGYGAVLFVENVL 300

QY 287 KDKGSLKGKRCCLVSGAGNVAQYCAELLEKGAI VLSLSDSQYVYEPNGFTREQLQAVQ 346  
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QY 347 DMKKKNSARISYKSDTAVYVGDRLKPELDCQVDIAFPFCATQNEIDHDAELLIKHGC 406  
Db 361 DMKKKNSARISYKSDTAVYVGDRLKPELDCQVDIAFPFCATQNEIDHDAELLIKHGC 420

QY 407 QYVVEGANPSTNEAIIHKYNKAGIICPGKAANAGGAVVSGLEMTQNRMSLNWTRREVRD 466  
Db 421 QYVVEGANPSTNEAIIHKYNKAGIICPGKAANAGGAVVSGLEMTQNRMSLNWTRREVRD 480

QY 467 KLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQAV 512  
Db 481 KLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAQAV 526

RESULT 5  
US-08-541-033A-24  
Sequence 24, Application US/08541033A  
Patent No. 5879941

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; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,033A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UF155
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-541-033A-24

Query Match 95.1%; Score 2508; DB 2; Length 487;
Best Local Similarity 100.0%; Pred. No. 5.4e-223;
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 AVSLEEQISAMDATTGDFALQKAVKQMATKAGTEGLVHGINKPDPVROLLTEIFMKDPEQ 61
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Db 62 QEFMQAVREAVSLQPVPEKPELLPIPKQIIVEPERSVITFRVSWLDDAGNLQVNRGFRVQ 121
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Db 122 YSSAIGPYKGGIRFHPNSVNLTKMFLAPEQIFKNSLTTLPMGGKGSGDFDPKGSDAEV 181
Qy 207 MRFCSFMTELQRHISYVDVPAGDIGVGAREIGVLFQYKRITKNYTGVLTPKQEGYGG 266
Db 182 MRFCSFMTELQRHISYVDVPAGDIGVGAREIGVLFQYKRITKNYTGVLTPKQEGYGG 241
Qy 267 SEIRPEATGYGAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLEKGAIIVLSLSD 326
Db 242 SEIRPEATGYGAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLEKGAIIVLSLSD 301
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Db 362 CATONEIDSHDAELIKHGCQVVEGANMPSNEAIHKYNKAGIIVCPGKAANAGVAVS 421
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Db 422 GLEMTQNRMSLNTWREVRDKLERIMKDIYDSAMGPSRRYNYDLAAGANIAGFTTKVADAV 481

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Qy 507 KAQNAV 512
Db 482 KAQNAV 487

RESULT 6
US-08-828-451-24
; Sequence 24, Application US/08828451
; Patent No. 5985634
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,451
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,033
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UF155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-828-451-24

Query Match 95.1%; Score 2508; DB 2; Length 487;
Best Local Similarity 100.0%; Pred. No. 5.4e-223;
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 AVSLEEQISAMDATTGDFALQKAVKQMATKAGTEGLVHGINKPDPVROLLTEIFMKDPEQ 86
Db 2 AVSLEEQISAMDATTGDFALQKAVKQMATKAGTEGLVHGINKPDPVROLLTEIFMKDPEQ 61
Qy 87 QEFMQAVREAVSLQPVPEKPELLPIPKQIIVEPERSVITFRVSWLDDAGNLQVNRGFRVQ 146
Db 62 QEFMQAVREAVSLQPVPEKPELLPIPKQIIVEPERSVITFRVSWLDDAGNLQVNRGFRVQ 121
Qy 147 YSSAIGPYKGGIRFHPNSVNLTKMFLAPEQIFKNSLTTLPMGGKGSGDFDPKGSDAEV 206
Db 122 YSSAIGPYKGGIRFHPNSVNLTKMFLAPEQIFKNSLTTLPMGGKGSGDFDPKGSDAEV 181
Qy 207 MRFCSFMTELQRHISYVDVPAGDIGVGAREIGVLFQYKRITKNYTGVLTPKQEGYGG 266
Db 182 MRFCSFMTELQRHISYVDVPAGDIGVGAREIGVLFQYKRITKNYTGVLTPKQEGYGG 241
Qy 267 SEIRPEATGYGAVLFVENVLKDGESLKGKRCCLVSGAGNVAQYCAELLEKGAIIVLSLSD 326

```

Db 242 SEIRPEATGYGAVLFVENVLKDKGESLKGKRCCLVSGAGNVAQYCAELLEKGAIVLSLSD 301  
QY 327 SQGYVYEPNGFTREQLQAVQDMKKONNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFP 386  
Db 302 SQGYVYEPNGFTREQLQAVQDMKKONNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFP 361  
QY 387 CATONEIDEHDAELLKHGCOYVVEGANPSTNEAIHKYNKAGIICPGKKAANAGGVAYS 446  
Db 362 CATONEIDEHDAELLKHGCOYVVEGANPSTNEAIHKYNKAGIICPGKKAANAGGVAYS 421  
QY 447 GLEMTQNRSLNWTREVRDKLERIMKDIYDSAMGPSRRYVNDVLAAGANIAGFTKVVADAV 506  
Db 422 GLEMTQNRSLNWTREVRDKLERIMKDIYDSAMGPSRRYVNDVLAAGANIAGFTKVVADAV 481  
QY 507 KAQAV 512  
Db 482 KAQAV 487

RESULT 7

US-08-541-033A-26  
; Sequence 26, Application US/08541033A  
; Patent No. 5879941  
; GENERAL INFORMATION:  
; APPLICANT: Schmidt, Robert R.  
; APPLICANT: Miller, Philip  
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
; TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE  
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/541,033A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Whitlock, Ted W.  
; REGISTRATION NUMBER: 36,965  
; REFERENCE/DOCKET NUMBER: UF155  
; TELEPHONE: (904) 375-8100  
; TELEFAX: (904) 372-5800  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 476 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-541-033A-26

Query Match 93.4%; Score 2465; DB 2; Length 476;  
Best Local Similarity 100.0%; Pred. No. 4.9e-219;  
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 37 MDATTGDTALQKAVQKMATKAGTEGLVHGKINPQVRLLTETFMKDPQEQBFMQAVREV 96  
Db 1 MDATTGDTALQKAVQKMATKAGTEGLVHGKINPQVRLLTETFMKDPQEQBFMQAVREV 60  
QY 97 AVSLQPVPEKRPPELLPIFKQIVPEPVRVITFRVSWLDDAGNLQVNRGFRVOYSSAIGPYKG 156  
Db 61 AVSLQPVPEKRPPELLPIFKQIVPEPVRVITFRVSWLDDAGNLQVNRGFRVOYSSAIGPYKG 120

QY 157 GLRPHPSVNLSTMKFLAFEQIFKNLSLTLLPMGGGKGGSDFDPKGKSDAEVMMRFQCSFMTE 216  
Db 121 GLRPHPSVNLSTMKFLAFEQIFKNLSLTLLPMGGGKGGSDFDPKGKSDAEVMMRFQCSFMTE 180  
QY 217 LORHSIYYQDVDPAGDIGVAREIGYLFQYKRITKNYTGVLTPKGOEYCGSEIRPEATGY 276  
Db 181 LORHSIYYQDVDPAGDIGVAREIGYLFQYKRITKNYTGVLTPKGOEYCGSEIRPEATGY 240  
QY 277 GAVLFVENVLKDKGESLKGKRCCLVSGAGNVAQYCAELLEKGAIVLSLSDSQGYVYEPNG 336  
Db 241 GAVLFVENVLKDKGESLKGKRCCLVSGAGNVAQYCAELLEKGAIVLSLSDSQGYVYEPNG 300  
QY 337 FTREQLQAVQDMKKONNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPQATONEIDEH 396  
Db 301 FTREQLQAVQDMKKONNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPQATONEIDEH 360  
QY 397 DAELLIKHGCOYVVEGANPSTNEAIHKYNKAGIICPGKKAANAGGVAVSGLEMTQNRMS 456  
Db 361 DAELLIKHGCOYVVEGANPSTNEAIHKYNKAGIICPGKKAANAGGVAVSGLEMTQNRMS 420  
QY 457 LNWTRREEVRDKLERIMKDIYDSAMGPSRRYVNDVLAAGANIAGFTTKVADAVKAQAV 512  
Db 421 LNWTRREEVRDKLERIMKDIYDSAMGPSRRYVNDVLAAGANIAGFTTKVADAVKAQAV 476

RESULT 8

US-08-828-451-26  
; Sequence 26, Application US/08828451  
; Patent No. 5985634  
; GENERAL INFORMATION:  
; APPLICANT: Schmidt, Robert R.  
; APPLICANT: Miller, Philip  
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
; TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE  
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/828,451  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/541,033  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Whitlock, Ted W.  
; REGISTRATION NUMBER: 36,965  
; REFERENCE/DOCKET NUMBER: UF155  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (904) 375-8100  
; TELEFAX: (904) 372-5800  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 476 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-828-451-26

Query Match 93.4%; Score 2465; DB 2; Length 476;  
Best Local Similarity 100.0%; Pred. No. 4.9e-219;  
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 MDATTGDTALOKAVQKATKAGTGLVHGIKNPDVRLQLLTFIMKDPQOEPMQAVREV 96  
Db 1 MDATTGDTALOKAVQKATKAGTGLVHGIKNPDVRLQLLTFIMKDPQOEPMQAVREV 60  
QY 97 AVSLQPVPEKRPPELLPIPKQIIVEPVRVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 156  
Db 61 AVSLQPVPEKRPPELLPIPKQIIVEPVRVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120  
QY 157 GLRFPSPVNLSTMKFLAEPQIFKNSLTTLPMGGGKGGSDPDPKGSDAEVRMPCQSPMTE 216  
Db 121 GLRFPSPVNLSTMKFLAEPQIFKNSLTTLPMGGGKGGSDPDPKGSDAEVRMPCQSPMTE 180  
QY 217 LQRHLSYVDVPAGDIGVAREIGYLFQYKRITKNYTGVLTPKQOEGGSEIRPEATGY 276  
Db 181 LQRHLSYVDVPAGDIGVAREIGYLFQYKRITKNYTGVLTPKQOEGGSEIRPEATGY 240  
QY 277 GAVLFVENVLDKGBSLKGRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQYVYEPNG 336  
Db 241 GAVLFVENVLDKGBSLKGRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQYVYEPNG 300  
QY 337 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAPPQATQNEIDEH 396  
Db 301 FTREQLQAVQDMKKKNSARISEYKSDTAVYVGDRRKPWELDCQVDIAPPQATQNEIDEH 360  
QY 397 DAELLIKHGCQVYVSGANMPSTNEAIHKYNKAGIICPGKAANAGGAVSGLMNTQNRMS 456  
Db 361 DAELLIKHGCQVYVSGANMPSTNEAIHKYNKAGIICPGKAANAGGAVSGLMNTQNRMS 420  
QY 457 LNWTRREVRDKLERIMKDIYDSAMPSPRRYVVDLAAGANIAGFTKVDADAVKAQGV 512  
Db 421 LNWTRREVRDKLERIMKDIYDSAMPSPRRYVVDLAAGANIAGFTKVDADAVKAQGV 476

## RESULT 9

US-09-252-991A-20646  
; Sequence 20646, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 20646  
; LENGTH: 450  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-20646

Query Match 49.6%; Score 1309; DB 4; Length 450;  
Best Local Similarity 59.2%; Pred. No. 3e-112;  
Matches 263; Conservative 55; Mismatches 120; Indels 6; Gaps 4;  
QY 72 VROLLTEIFMKDPQOEPMQAVREVAVSLQPVPEKRPPELLP--IFKQIIVEPVRVITFRVS 129  
Db 10 VDAFLERLKRDPDQEPFHQAEEVRLSLWPPLEANPHYLEAGIIEIVEPERALLFRVP 69  
QY 130 WLDDAGNLQVNRGFRVQYSSAIGPYKGLRFPSPVNLSTMKFLAEPQIFKNSLTTLPMGG 189  
Db 70 WYDDQGRVRNRGFRVQYSSAIGPYKGLRFPSPVNLSTMKFLAEPQIFKNSLTTLPMGG 129  
QY 190 KGGGSDPDPKGSDAEVRMPCQSPMTELRHISYVQDVPAGDIGVAREIGYLFQYKRI 249  
Db 130 KGGGSDPDPKGSDAEVRMPCQSPMTELRHISYVQDVPAGDIGVAREIGYLFQYKRL 189  
QY 250 TKNYTGVLTPKQOEGGSEIRPEATGYGAVLFVENVLDKGBSLKGRCLVSGAGNVAQY 309

Db 190 SNQFTSVLTGKLSYGSLIRPEATGFCVYFAQEMLKDRCRGDPGQRVAISGSGNVAQY 249  
QY 310 CAELLLEKGAIVLSLSDSQYVYEPNGFTREQLQAVQDMKKKNSARISEYKSDTAVYV 369  
Db 250 AARKVMEGKGKVISLSDSBEGTLYAEAGLSDBQEWYLMELKNVRR-GRIREMAEQPSLQFL 308  
QY 370 DRRKPWELDCQVDIAPPQATQNEIDEHDAELLIKHGCQVYVSGANMPSTNEAIHKYNKAG 429  
Db 309 EGRRPWGLAC--DIALPCATQNEIDARLLANGCVCVABGANMPSTLEAVDLFLEAG 366  
QY 430 ILYCPGKAANAGGAVSGLMNTQNRMSLNWTRREVRDKLERIMKDIYDSA-MGPSRRYV 488  
Db 367 ILYAPGKASNAGGAVSGLMNSQAMRLRWSEGEVDYKLHGIMQSIHACILLYGEEQGRV 426  
QY 489 DLAAGANIAGFTKVDADAVKAQGV 512  
Db 427 NYVKGANIAGFVKVADAMLAQGV 450  
RESULT 10  
US-09-328-352-5725  
; Sequence 5725, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 5725  
; LENGTH: 467  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-5725

Query Match 47.7%; Score 1257.5; DB 4; Length 467;  
Best Local Similarity 55.9%; Pred. No. 1.9e-107;  
Matches 256; Conservative 61; Mismatches 128; Indels 13; Gaps 5;  
QY 63 LVH-----GKNPDPVRLQLLTFIMKDPQOEPMQAVREVAVSLQPVPEKRPPELLP--IF 114  
Db 11 LIHYAEDRAIKYNNLNEFLNYVQARDPHQEPFLQAVEEVTSLWPFIEKQPEVAEQGLL 70  
QY 115 KQIIVEPVRVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGLRFPSPVNLSTMKFLAF 174  
Db 71 ERLVEPVRVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGLRFPSPVNLSTMKFLAF 130  
QY 175 EQIFKNSLTTLPMGGGKGGSDPDPKGSDAEVRMPCQSPMTELRHISYVQDVPAGDIGV 234  
Db 131 EQTFKNSLTTLPMGGGKGGSDPDPKGSDAEVRMPCQSPMTELRHISYVQDVPAGDIGV 190  
QY 235 GAREIGYLFQYKRITKNYTGVLTPKQOEGGSEIRPEATGYGAVLFVENVLDKGBSLK 294  
Db 191 GAREVGMAGMMKKLSNDTACVFTGKGISFGSLMRPEATGYGVYFAEMLKTRGQSPA 250  
QY 295 GKRCVLVSGAGNVAQYCAELLLEKGAIVLSLSDSQYVYEPNGFTREQLQAVQDMKKKNS 354  
Db 251 KGTVSISSGSGNVAQYAAEAKAMFLGAKVVLSDSNGTVYVKNPDTDELLAEVMEKLNKR- 309  
QY 355 ARISEYKSDTAVYVGDRRKPWELDCQVDIAPPQATQNEIDEHDAELLIKHGCQYVVEGAN 414  
Db 310 GRISSEFASKHGFYEPGKTPMHI--PVDIALPCATQNEIDTGEDAKTLIANGVICVAEGAN 367  
QY 415 MPSTNEAIHKYNKAGIICPGKAANAGGAVSGLMNTQNRMSLNWTRREVRDKLERIMK 474  
Db 368 MPSTLEAVEHFIEAKILYAPKASNAGGAVSGLMNSQAMRLRWSEGEVDYKLHGIMQSIHACILLYGEEQGRV 427  
QY 475 IYDSAM--GPSRRYVVDLAAGANIAGFTKVDADAVKAQGV 510  
Db 428 IHANCVRYGTGEDGTVNYVDGANIAGFVKVADAMLAQGV 465





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; FILING DATE: 01-JUL-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/021,058
; FILING DATE: 02-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kokulis, Paul K.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 81163/241766
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)-861-3503
; TELEFAX: (202)-822-0944
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 447 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
US-08-886-640-3

```

```

Query Match 45.5%; Score 1201; DB 2; Length 447;
Best Local Similarity 54.0%; Pred. No. 2.9e-102;
Matches 241; Conservative 67; Mismatches 128; Indels 10; Gaps 5;

QY 72 VQLLLEIFMKDPEQOEPMQAVREAVSLQPVFEKPEL--LPFKQIVPERVITFRVS 129
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 7 LESFLNHVQRDPNQTPEFAQAVREVTMTLWPFLEQNPKYRQMSLLERLVEPERVIOFRV 66
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 130 WLDADGNLQVNRFRVQYSSAIGPYKGLRPHSPVNLISIMKFLAPEQIPKNSLTTLPMGG 189
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 67 WDDRNQIQVNRAMRVQFSSAIGPYKGNRFHPSVNLISILKFLGEQTFKNALITLPMGG 126
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 190 KGKGSDFDPKGSDAEVMRFQCSFMTELORHISYVDVPAGDIGVGAREIGYLFQYKRI 249
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 127 KGKGSDFDPKGSSEGVNRFQALMTLEYRHLGADTDVPAGDIGVGREGVGMAGMMKKL 186
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 250 TKNYTGVLTTPKQOEYGGSEIRPEATGYCAVLFEVNLKDKGSLKGRCLVSGAGNVAQY 309
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 187 SNNTACVFTGKLSFGSLIRPEATGYGLVYFTTEAMLRKHGMFGFEGMRVSVSGGNVAQY 246
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 310 CAELLEKGAIVLSLSDSGYVYEPNGFTREOLQAVQDMKKNNNSARISEYKSDTAVYVG 369
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 247 ALEKAMEFGARVITASDSGTVVDESGETKEKLARLIEI-KASRGRVADYAKEGLVYL 305
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 370 DRKRWELDCQVDIAPPQATONEIDEHDAELIKHGCOYVVEGANMPSTNEAIHKYNKAG 429
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 306 EQQPMWLSL--PVDIALPCATQNELDVDAHQIANGVKAABEGANMPTTIEATELFPQAG 363
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 430 ILYCPKKAANAGGAVSGLEMTQNRMSLNWTREVRDKLERIMKDIYDSAM---GPSRRY 486
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 364 VLFAFGKAANAGGAVATSGLEMAQNAARLGWKAEBKVDARLHHIMLDIHHCVDHGGEQGT 423
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 487 NVDLAAGANIAGFTKVADAVKAQAGV 512
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 424 N--YVQGANIAGFVKVADAMLQAGVI 447
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 14
US-08-884-235-11
; Sequence 11, Application US/08884235
; Patent No. 6329573
; GENERAL INFORMATION:
; APPLICANT: Lightfoot, David A.
; APPLICANT: Long, Lynn M.
; APPLICANT: Lightfoot, Maria E. Vidal
; TITLE OF INVENTION: PLANTS CONTAINING THE gdhA GENE AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington

```

```

; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/884,235
; FILING DATE: 27-JUN-1997
; CLASSIFICATION: 800
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 447 residues
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
US-08-884-235-11

```

```

Query Match 45.5%; Score 1201; DB 3; Length 447;
Best Local Similarity 54.0%; Pred. No. 2.9e-102;
Matches 241; Conservative 67; Mismatches 128; Indels 10; Gaps 5;

QY 72 VQLLLEIFMKDPEQOEPMQAVREAVSLQPVFEKPEL--LPFKQIVPERVITFRVS 129
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 7 LESFLNHVQRDPNQTPEFAQAVREVTMTLWPFLEQNPKYRQMSLLERLVEPERVIOFRV 66
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 130 WLDADGNLQVNRFRVQYSSAIGPYKGLRPHSPVNLISIMKFLAPEQIPKNSLTTLPMGG 189
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 67 WDDRNQIQVNRAMRVQFSSAIGPYKGNRFHPSVNLISILKFLGEQTFKNALITLPMGG 126
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 190 KGKGSDFDPKGSDAEVMRFQCSFMTELORHISYVDVPAGDIGVGAREIGYLFQYKRI 249
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 127 KGKGSDFDPKGSSEGVNRFQALMTLEYRHLGADTDVPAGDIGVGREGVGMAGMMKKL 186
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 250 TKNYTGVLTTPKQOEYGGSEIRPEATGYCAVLFEVNLKDKGSLKGRCLVSGAGNVAQY 309
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 187 SNNTACVFTGKLSFGSLIRPEATGYGLVYFTTEAMLRKHGMFGFEGMRVSVSGGNVAQY 246
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 310 CAELLEKGAIVLSLSDSGYVYEPNGFTREOLQAVQDMKKNNNSARISEYKSDTAVYVG 369
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 247 ALEKAMEFGARVITASDSGTVVDESGETKEKLARLIEI-KASRGRVADYAKEGLVYL 305
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 370 DRKRWELDCQVDIAPPQATONEIDEHDAELIKHGCOYVVEGANMPSTNEAIHKYNKAG 429
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 306 EQQPMWLSL--PVDIALPCATQNELDVDAHQIANGVKAABEGANMPTTIEATELFPQAG 363
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 430 ILYCPKKAANAGGAVSGLEMTQNRMSLNWTREVRDKLERIMKDIYDSAM---GPSRRY 486
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 364 VLFAFGKAANAGGAVATSGLEMAQNAARLGWKAEBKVDARLHHIMLDIHHCVDHGGEQGT 423
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 487 NVDLAAGANIAGFTKVADAVKAQAGV 512
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 424 N--YVQGANIAGFVKVADAMLQAGVI 447
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 15
US-08-370-193A-11
; Sequence 11, Application US/08370193A
; Patent No. 5573945
; GENERAL INFORMATION:
; APPLICANT: ONO, EIJI
; APPLICANT: TSUJIMOTO, NOBUHARU
; APPLICANT: MATSUI, KAZUHIKO
; APPLICANT: KURAHASHI, KAZUHIKO
; TITLE OF INVENTION: MUTANT AND METHOD FOR PRODUCING
; TITLE OF INVENTION: L-GLUTAMIC ACID BY FERMENTATION
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.

```

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/370,193A  
FILING DATE: 09-JAN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 10-714-0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 447 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-370-193A-11

Query Match 45.5%; Score 1200; DB 1; Length 447;  
Best Local Similarity 54.0%; Pred. No. 3.6e-102;  
Matches 241; Conservative 67; Mismatches 128; Indels 10; Gaps 5;  
QY 72 VRLQLTEIFMKDPEQOEFMQAVREAVSLQPVFEKEPEL--LP1FKQIVPEPVRVITFRYS 129  
Db 7 LESFLNHVQRPDPNQTEFAQAVREVTTLWPFLEQNPKYRQMSLLERLVEPVRVIOFRVY 66  
QY 130 WLDDAGNLQVNRGRFRVQYSSAIGPYKGLRFPSPVNLISIMKFLAFQIFKNSILTLIPMG 189  
Db 67 WDDRNQIQVNRARVQPSAIGPYKGNRFPSPVNLISILKFLGFEQTFKNALTTLIPMG 126  
QY 190 GKGGSDFDPKGSDDAEVMPFCOSFMTELQRHSYVQDVPAGDIGVGAREIGYLFQYKRI 249  
Db 127 GKGGSDFDPKGSSEGVMEFQALMTELYRHLGADTDVPAGDIGVGREVGFMAGMMKXL 186  
QY 250 TKNYTGVLTPKGOEYCGSEIRPEATGYGAVLPVENVLKDGESLKGKRCCLVSGAGNVAQY 309  
Db 187 SNTACVFTGKGLSFGGSLIRPEATGYGLVYFTEAMLKRHGMFGEMRVSVSGGNVAQY 246  
QY 310 CAELLLEKGAIVLSLSDSQGYVVEPNQFTREOLOAVODMKKNNSARISEYKSDTAVVYG 369  
Db 247 AIEKAMEFGARVITASDSSGTVDSESGFTREKLARLIEI-KASRGRVADYAKEFGLVYL 305  
QY 370 DRKRWELPCQVDIAFPCCATQNEIDHDAELIHKGCQYVVEGANMPSTNEAIHKYNKAG 429  
Db 306 EQQPMWLS--PVDIALPCATQNELDVAHAQLIANGVAKAVEGANMPTTIEATELFFQQAG 363  
QY 430 IYFCGKAANAGVAVSGLEMTQNRMSLNWTRREVRDKLERIMKOIYDSAM---GPSRRY 486  
Db 364 VLFAPGKAANAGGVATSGLEMPQNAARLGLWKAQKVDARLHIMLDITHACVEHGEGET 423  
QY 487 NVDLAAGANIAGFTKVADAKQAGAV 512  
Db 424 N--YVQGANIAGFVKVADAMLAQGI 447

Search completed: September 8, 2005, 02:12:06  
Job time : 30.4224 secs

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Query Match 48.8%; Score 1286.5; DB 2; Length 470;  
Best Local Similarity 55.2%; Pred. No. 8e-79; Indels 19; Gaps 7;  
Matches 266; Conservative 64; Mismatches 133;  
Qy 34 ISAMDATTDFTALQAVKQMATKAGTEGLVHGINKPDRROLTEIFMKDPCQOEPMQAV 93  
Db 1 MALADKOTGRFVVLDR-----NASVYESTLV-----DQENNNYERMKLDPRQVETLQAF 50  
Qy 94 REVANSLOQVEFEKRPBLLPIFKQIYEPPEVITFRVSWLDDAGNLQVNRGRVOYSSAIDP 153  
Db 51 HEILVSLKEDLFMEPEPKYLPILIELTSEPERAIOFRVCLMDNGVQRKRCFRVQYNSALGP 110  
Qy 154 YKGGARFHSVNLSTIMKFLAFEOIFKNSLTTLPMGGCKGSDPDPKGSADAEVMPRCOSF 213  
Db 111 YKGGARFHSVNLSTIVKFLAFEOIFKNSLTGLSMGGCKGSDPDPKGSADAEVMPRCOSF 170  
Qy 214 MTELQHSISYVDVPAADIGVAREIGVLFQGYKRTTKNYTGYLTPKGOEYGSSEIRPA 273  
Db 171 KMELVYHIGPCTDVPAGDIGVGREIGVLYGYKKIVNSPNTGLTKNVMGGSNLRVZA 230  
Qy 274 TGYGAVLFPEVNLKDKGBSLKGRCLVSGAGVAVQYCAELLLEKALVLSDSQGYVE 333  
Db 231 TGYGAVLFPEVNLKDKGBSLKGRCLVSGAGVAVQYCAELLLEKALVLSDSQGYVE 290  
Qy 334 PNGFTREOLQAVQDMKKKNSARISFY--KSDTAVVGDGRKRPWELDCQVDIAFPATON 391  
Db 291 PNGFTRENLLEFLDLKEE--KKGRIKSYLNHSSYAKYF--DNEKRWGVC--TLAFCATON 346  
Qy 392 EIDEDHAEILLIKGCQYVEGAMNPSTNEAIHKYKAGIYCPGKANAGVAVSGLEMT 451  
Db 347 EINLDEAKLLQKNGCLVGEANMPSTVDALNIFKSNNTIYCPSKANAGVAVISGLEMS 406  
Qy 452 QNRMSLNTREBYRDKLERIMKDIYDAMGPSRRY--NVDLAAGANIAGFTKVADAVKA 508  
Db 407 QNFQESHMTREYDEKLKEIMENIIFACSENLKTYKNKYDLOAGANIAGFLKVAESYIE 466  
Qy 509 OG 510  
Db 467 OG 468  
RESULT 13  
Qy 0923C4 PRELIMINARY; PRT; 445 AA.  
AC 0923C4,  
DT 01-MAY-1999 (Tremblrel). 10, Created  
DT 01-MAY-1999 (Tremblrel). 10, Last sequence update  
DT 05-JUL-2004 (Tremblrel). 27, Last annotation update  
DE NADP-glutamate dehydrogenase (BC 1.4.1.4).  
GN Name-gdh;  
OS Pseudomonas aeruginosa.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=287;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PAC1;  
RA Ansaari F.;  
RA Theiss (1994), University of London London U.K.  
RL Theiss (1994), University of London London U.K.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PAC1, and PAOI;  
RA Brown P.R.;  
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PAOI;  
RA Ansaari F.;  
RA Theiss (1994), University of London, London U.K.  
RL EMBL; Y18494; CAA71192.1; -  
DR EMBL; Y15166; CAA75437.1; -  
DR HSSP; P24295; IADP.  
DR GO; GO:0004354; F:glutamate dehydrogenase (NADP+) activity; IEA.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0006520; P:amino acid metabolism; IEA.  
DR InterPro; IPR006095; GLFV\_dehydrog.  
DR InterPro; IPR006096; GLFV\_dehydrog\_C.  
DR InterPro; IPR006097; GLFV\_dehydrog\_N.  
DR Pfam; PF00208; GLFV\_dehydrog; 1.  
DR Pfam; PF02812; GLFV\_dehydrog\_N; 1.  
DR PRINTS; PR00082; GLFVDRKGNSE.  
DR PROSITE; PS00074; GLFV\_DEHYDROGENASE; 1.  
DR Oxioreductase.  
SQ SEQUENCE 445 AA; 48532 MW; B00DD8E03A06D8A CRC64;  
Query Match 48.7%; Score 1285; DB 2; Length 445;  
Best Local Similarity 58.4%; Pred. No. 9.4e-79;  
Matches 261; Conservative 56; Mismatches 118; Indels 12; Gaps 5;  
Qy 72 VROLTEIFMKDPEQOEPMQAVREVAVALQVFEKRPBLLP--IPKQIYEPPEVITFRVS 129  
Db 5 VDAFLERLKRDPDPPEFHQAVEBVLRLMFLFLEANPHYLEAGITERLVEPERAILFFVP 64  
Qy 130 WDDAGNLQVNRGRFRVOYSSAIGPYKGLRFRHPSVNLSTIMKFLAFEOIFKNSLTTLPMGG 189  
Db 65 WDDQGRVVRNRYGVQSSAIGPYKGLRFRHPSVNLGLKFLAFEOIFKNSLTTLPMGG 124  
Qy 190 GKGSDFDPKGSDEUNRFGQSPFTELQHSISYVDVPAADIGVAREIGVLFQGYRRL 249  
Db 125 GKGSDFDPKGSDEUNRFGQSPFSELYRVAGDLVPADIGVAREIGVLFQGYRRL 184  
Qy 250 TKNYTGVLTPKGOEYGSSEIRPEATGYAVLFVENVLKDKBSLKGRCLVSGAGVAVQY 309  
Db 185 SNQFISVLTGKGLSTGGSLIRPEATGFCYVFAQMLDNRGRGFRPGQAVLSGSANVQY 244  
Qy 310 CAELLLEKALVLSDSQGYVEPNFTREOLQAVQDMKKKNSARISSEYKSDT--AV 366  
Db 245 AARKVMENKGVKISTLSEDEGLTYAAGLSDEQWEYIMELK---NARAGHPRDGVEQPSL 300  
Qy 367 YVGDGRKRPWELDCQVDIAFPATONEIDEDHAEILLIKGCQYVEGAMNPSTNEAIHKYN 426  
Db 301 QFLBGPVPMGLAC--DILPCATONELDAEDRRRLRANCCVAVGAMNPSTLEVDLFL 358  
Qy 427 KAGIYCPGKANAGVAVSGLEMTQNRMSLNTREBYRDKLERIMKDIYDAMGPSRRR 485  
Db 359 EAGIITYAGKASNMAGVAVSGLEMSQNMRLRMSGSEVDTLHGIMQSIHACLLYGBEQ 418  
Qy 486 YNVDLAAGANIAGFTKVADAVKAQGA 512  
Db 419 GRVNVKGANIAGFYKVADAMLAQGV 445  
RESULT 14  
Qy 07Y2U7 PRELIMINARY; PRT; 437 AA.  
AC 07Y2U7,  
DT 01-OCT-2003 (Tremblrel). 25, Created  
DT 01-OCT-2003 (Tremblrel). 25, Last sequence update  
DT 01-MAR-2004 (Tremblrel). 26, Last annotation update  
DE Glutamate dehydrogenase (Fragment).  
GN Name-gdh;  
OS Trichomonas vaginalis.  
OC Eukaryota; Parabasalia; Trichomonada; Trichomonadida;  
OC Trichomonadidae; Trichomonadinae; Trichomonas.  
OX NCBI\_TaxID=5722;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC PubMed=12820901; DOI=10.1186/1471-2148-3-14;  
RA Andersson J.O.; Roger A.J.;  
RT "Evolution of glutamate dehydrogenase genes: evidence for lateral gene transfer within and between prokaryotes and eukaryotes";  
RL BMC Evol. Biol. 3:14-14(2003).  
DR EMBL; AF533886; AAP83853.1; -  
DR HSSP; P24295; IADP.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0006520; P:amino acid metabolism; IEA.

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QY 190 GKGSDFDPKSKDAEYMRFCQSFMTLQHHISYVODVPAGDIGVAREIGYLFGQYKRI 249
DB 128 GKGSDFDPKSKDAEYMRFCQSFMTLQHHISYVODVPAGDIGVAREIGYLFGQYKRI 187
QY 250 TKNYTGLTPKGGSEYRPRATGGAULTFVBNYTKDGBSLKGRCLVSGAGNVAOY 309
DB 188 ANQFTSVLTKGMYTGSGLRPRATGCGYFAEBMLKRODKRI DGRVAVSGSGNVAOY 247
QY 310 CAELLEKGAIVLSLSDQGYVEPENGFTREQLQAVODMKKNNARSISEKSDTAVYVG 369
DB 248 AARKWDLGGKIVLSLSSECTIYAEAGLTQAWDMELKONVR -GRISLAQFGLEFR 306
QY 370 DRKPEWELDCQVDIAFPATONEIDEHDAELIKHGQCYVVEGAMNPSTNEAIHKYNKAG 429
DB 307 KQGTFWMLPC--DIALPCATONEIAGADARTLLRNGCICVABGANPPTLEAVDIFLDAG 364
QY 430 ILYCPGAANAAGVAVSGLEMTONRMSLMTREBYDKLERIMKDIYDSAM--GFSRRYV 487
DB 365 ILVAPGASNAAGVAVSGLEMSQNAKRLMTAGBVSCLKINMOSIHHACVHYGBRADGR 424
QY 488 VDLAAGANIAGFTKTVADAVAKAGAV 512
DB 425 INVYKGANINAGFTKTVADAMLAQGVV 449

RESULT 11
096940 PRELIMINARY; PRT; 470 AA.
ID 096940;
AC 096940;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DB 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DB Glutamate dehydrogenase (NADP+) (EC 1.4.1.4).
Name=GLUDH; Synonyms=GDH;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxId=5833;
RX MEDLINE=99089647; Pubmed=9874251;
RA Wagner J.T., Luedemann H., Faerber P.M., Lottspeich F.,
RA Krauch-Siegel R.L.;
RT "Glutamate dehydrogenase, the marker protein of Plasmodium falciparum.
RT Cloning, expression and characterization of the malarial enzyme.";
RL Bur. J. Biochem. 258:813-819(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Li J.H., Li M., Wu Y.S., Wang P.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DB EMBL; Y12927; CAA73390.1; -.
DB EMBL; AY040586; AAK77969.1; -.
DB HSSP; P24295; IADP.
DR GO; GO:0004354; F:glutamate dehydrogenase (NADP+) activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV_dehydrog_N.
DR InterPro; IPR006096; GLFV_dehydrog_C.
DR InterPro; IPR006097; GLFV_dehydrog_N.
DR Pfam; PF00208; GLFV_dehydrog_1.
DR Pfam; PF02812; GLFV_dehydrog_N_1.
DR PRINTS; PR00082; GLFVDRGNASE.
DR PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
KW Oxidoreductase.
SQ SEQUENCE 470 AA; 52546 MW; 50A37C23484C387A CRC64;

Query Match 48.8%; Score 1286.5; DB 2; Length 470;
Best Local Similarity 55.2%; Pred. No. 8e-79;
Matches 266; Conservative 64; Mismatches 133; Indels 19; Gaps 7;

QY 34 ISAMDITTDFTLQCAVQMAKATGEGYHGIKMPDVRLQTLTEIFMDPESQEMQAV 93
DB 1 MSALKDKTGRFVVLDR-----NASYSEIV-----DOENNVYERVKLDPNQVETLQAF 50
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QY 94 REVAVSLQPFKRPPELLPIFKQIVPERVITFRVSWLMDAGNLQVNRGFRVQYSSAIGP 153
DB 51 HEILVSLKTLFMEBPXYLLPIETLSPERALQFRVCMWLDNGVQRNKRFRVQYNALGP 110
QY 154 YKGGILFPHSVNLSTMKFLAFEOIFKNSLTTLPMGGCKGSDPDPKSKDAEYMRFCQSF 213
DB 111 YKGGILFPHSVNLSTYKFLGFEOIFKNSLTGLSMGCKGSDPDPKSKDNELTKCQAF 170
QY 214 MTELQHHISYVODVPAGDIGVAREIGYLFGQYKRI TKNYTGLTPKGGSEYRPR 273
DB 171 MTELQHHISYVODVPAGDIGVAREIGYLFGQYKRI VNSFNGTLTKNYKRVGSSNLRV 230
QY 274 TGYGAVLTFVBNYTKDGBSLKGRCLVSGAGNVAOYCAELLEKGAIVLSLSDQGYVE 333
DB 231 TGYGAVLTFVBNYTKDGBSLKGRCLVSGAGNVAOYCAELLEKGAIVLSLSDQGYVE 290
QY 334 PNGFTREQLQAVODMKKNNARSISEY--KSDTAVYVGGRRKPEWELDCQVDIAFPATON 391
DB 291 PNGFTREQLQAVODMKKNNARSISEY--KSDTAVYVGGRRKPEWELDCQVDIAFPATON 346
QY 392 EIDEHDAELIKHGQCYVVEGAMNPSTNEAIHKYNKAGIITCPGAANAAGVAVSGLEMT 451
DB 347 EIDEHDAELIKHGQCYVVEGAMNPSTNEAIHKYNKAGIITCPGAANAAGVAVSGLEMT 406
QY 452 QNRMSLMTREBYDKLERIMKDIYDSAMGFSRRY--NVDLAAGANIAGFTKTVADAVKA 508
DB 407 QNFPQSHMTREBYDKLERIMKDIYDSAMGFSRRY--NVDLAAGANIAGFTKTVADAVKA 466
QY 509 QG 510
DB 467 QG 468

RESULT 12
081170 PRELIMINARY; PRT; 470 AA.
ID 081170;
AC 081170;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DB NADP-specific glutamate dehydrogenase.
GN ORFNames=PP14_0164;
OS Plasmodium falciparum (Isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxId=36329;
RX MEDLINE=2255705; Pubmed=1236864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Patil A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.S., Nene V., Shallow S.O., Sun B., Peterson J., Angiuoli S.,
RA Pertea M., Allen J., Selengut J., Harte D., Mather M.W., Valdivia A.B.,
RA Martin D.M., Fairclark A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings I.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum."
RL Nature 419:498-511(2002).
DB EMBL; AE014818; AAN36776.1; -.
DB HSSP; P24295; IADP.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV_dehydrog_N.
DR InterPro; IPR006096; GLFV_dehydrog_C.
DR InterPro; IPR006097; GLFV_dehydrog_N.
DR Pfam; PF00208; GLFV_dehydrog_1.
DR Pfam; PF02812; GLFV_dehydrog_N_1.
DR PRINTS; PR00082; GLFVDRGNASE.
DR PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
SQ SEQUENCE 470 AA; 52546 MW; 50A37C23484C387A CRC64;
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|   |  |  |              |
|---|--|--|--------------|
| Db  | 302  | YFEKQKPGV--AAITALPCATQNLDEBAKTLTILANGCYVAEGANMSTIGAVBQFK       | 359          |
| Qy  | 428  | AGIYYCPGKANAGVAVSGLMTQNRSLNLTREBVRDKLRIMKDIYDSAMGSPRRY-        | 486          |
| Db  | 360  | AGILYAPKASNAAGVATISGLEMSQNAIRLSWTREBVRDRLFGIMQSIHESCL---       | KYG 415      |
| Qy  | 487  | ---NVDLAAGNINGFTPKADAVAAQ                                      | 510          |
| Db  | 416  | KVGDTVYVYVNGANIAGFTYKVAADAMLAQ                                 | 443          |
| RESULT 9  |  |  |              |
|   | 90J756   | PRELIMINARY;   | PRT; 444 AA. |
| AC  | 09J756;  |  |              |
| DT  | 01-OCT-2000 (TREMBLREL. 15, Created)                                   |  |              |
| DT  | 01-OCT-2000 (TREMBLREL. 15, laet sequence update)                      |  |              |
| DT  | 01-OCT-2003 (TREMBLREL. 25, laet annotation update)                    |  |              |
| DE  | Glutamate dehydrogenase (EC 1.4.1.4).                                  |  |              |
| GN  | Name=gdba; OrderedlocusNames=MNA1964;                                  |  |              |
| OS  | Neisseria meningitidis (serogroup A).                                  |  |              |
| OC  | Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;            |  |              |
| OC  | Neisseriaceae; Neisseria.  |  |              |
| OX  | NCBI_TaxID=65699;  |  |              |
| RN  | [1]  |  |              |
| RP  | SEQUENCE FROM N.A.   |  |              |
| RC  | STRAIN=Z2491 / Serogroup A / Serotype 4A;                              |  |              |
| RX  | MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;               |  |              |
| RA  | Parthali J., Achman M., James K.D., Bentley S.D., Churcher C.M.,       |  |              |
| RA  | Klee S.H., Morelli G., Basham D., Brown D., Chillingworth T.,          |  |              |
| RA  | Davies R.M., Davis P., Devlin K., Fentwell T., Hamlin N., Holtroyd S., |  |              |
| RA  | Jagels K., Leather S., Moulé S., Mungall K.L., Quail M.A.,             |  |              |
| RA  | Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,             |  |              |
| RA  | Whitehead S., Spratt B.G., Barrett B.G.,                               |  |              |
| RT  | "Complete DNA sequence of a serogroup A strain of Neisseria            |  |              |
| RT  | meningitidis Z2491."   |  |              |
| RL  | Nature 404:502-506 (2000).   |  |              |
| DR  | EMBL; AL162757; CAB85184.1; -.   |  |              |
| DR  | PIR; B81825; B81825.   |  |              |
| DR  | HSSP; P24295; IADP.  |  |              |
| DR  | GO; GO:0004354; F:glutamate dehydrogenase (NADP+) activity; IEA.       |  |              |
| DR  | GO; GO:0016493; F:oxidoreductase activity; IEA.                        |  |              |
| DR  | GO; GO:0006520; P:amino acid metabolism; IEA.                          |  |              |
| DR  | InterPro; IPR006095; GLFV dehydrog.                                    |  |              |
| DR  | InterPro; IPR006096; GLFV dehydrog. C.                                 |  |              |
| DR  | InterPro; IPR006097; GLFV dehydrog. N.                                 |  |              |
| DR  | Pfam; PF00208; GLFV dehydrog. N; 1.                                    |  |              |
| DR  | Pfam; PF02812; GLFV dehydrog. N; 1.                                    |  |              |
| DR  | PRINTS; PR00082; GLFDHGNASE.   |  |              |
| DR  | PROSITE; PS00074; GLFV DEHYDROENASE; 1.                                |  |              |
| KW  | Complete proteome; Oxidoreductase.                                     |  |              |
| SQ  | SEQUENCE 444 AA; 48462 MW; DE7FLA7B8DD6f424 CRC64;                     |  |              |
| Query Match 49.1%; Score 1294.5; DB 2; Length 444;              |  |  |              |
| Best Local Similarity 57.1%; Pred. No. 2.1e-79;                 |  |  |              |
| Matches 256; Conservative 72; Mismatches 105; Indels 15; Gaps 6 |  |  |              |
| Qy  | 71   | DVROCLTEIFMDPEQOEFMQAVREAVVSLQPFERKPELT--PIKQIVPERVITFRV       | 128          |
| Db  | 3  | DLNTLIPANLKQNPDPERPHQAVEVFVMSLDPLAIPKPYTQGSLLRIEYPERVAFV       | 62           |
| Qy  | 129  | SWLDDAGNLQVNRGRFVQYSSAIGPKKGLRFRPVSNSIMKTLAEQIFKNSLTLLPMG      | 188          |
| Db  | 63   | TWQDDKGOVQVNRGRVQWSSAIGPKKGLRFRPVTDLGVLFKFLAEQVFKNALITLLPMG    | 122          |
| Qy  | 189  | GSGKGSDFPKPKSKDAEAVRFQCSFWTELORHISYVDVPADGIDIGAGAREIGLFGQYKR   | 248          |
| Db  | 123  | GSGKGSDFPKPKSKDAEAVRFQCAFPTTELYRHHGADTDVPAGDIDIGAGAREIGLFGQYKR | 182          |
| Qy  | 249  | ITKNTGTGVLTPYQGEYGSSEIRPEATGYAVLFENVLYLKDKGSLKGRCLVSGAGNVAQ    | 308          |
| Db  | 183  | INRNSFVLTQKGLKMGSLIRPEALGYGVVFAQMLQYRNDSPGKRTVLSGSGNVAQ        | 242          |

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QY 309 CCAETLLEKKAIVLSTLSGQGVYER -NGFTREQLQAVODMKKKNNNAISISKSTPAY 367
Db 243 YAAEAGAIQLGAKVLVSDSNGVFLFPDSGMSQAQLALILEVRR -RVATYAKGQGLQ 301
QY 368 VGDRRKPEMLCCOVDIAFPFCAQNEIDSHDALLIKGQCVVEGAMNPSTYEAIRKYNK 4277
Db 302 YFENQKPGV--AAEIALPCATQNLDBEAKKTLILANGCVVAEAGNMSTIGAVGPIK 359
QY 428 AGIITYPCGKAAAGVAVSGLEMTQNRMSLMTREERVDKLERIMKDIYDSANGSPRRY- 486
Db 360 AGIIVAPKASAGAGVATSGLEMSQNAIRLSTWREEVQRLFGIMQS IHESCL---KYG 415
QY 487 ----NVDLAACANATGPTKVDAYVAAG 510
Db 416 KVGDVTNVTYVNGANIAGFVKVADPAMLAQG 443

RESULT 10
088023
ID 088023 PRELIMINARY; PRT; 449 AA.
AC 088023;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Glutamate dehydrogenase.
GN Name=gdhA; OrderedLocustNames=PF0675;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22423060; PubMed=12534463.
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L.M., Beanan M.J., Deboy R.T., Daugherty S.C., Kolonay J.F.,
RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
RA Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
RA Moazzer A., Uetebach I.R., Rizzo M., Lee K., Kosack D., Woestei D.,
RA Wedler H., Lamber J., Stjepandic D., Hohnsbeil J., Streletz M., Helm S.,
RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuenmiller B.,
RA Frazer C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440.";
RL Environ. Microbiol. 4:799-808(2002).
DR EMBL; AE016776; AAN66300.1; -.
DR HSSP; P24295; IAUU.
DR TIGR; PP0675; -.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0005520; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV_dehydrog.
DR InterPro; IPR006096; GLFV_dehydrog_C.
DR InterPro; IPR006097; GLFV_dehydrog_N.
DR Pfam; PF00208; GLFV_dehydrog_1.
DR Pfam; PF02812; GLFV_dehydrog_1.
DR PRINTS; PR00082; GLFHDGNSAE.
DR PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
KW Complete proteome.
SQ SEQUENCE 449 AA; 48871 MW; EF1733B6ABC89627 CRC64;

Query Match 48.8%; Score 1287.5; DB 2; Length 449;
Best Local Similarity 58.2%; Pred. No. 6.4e-79;
Matches 259; Conservative 55; Mismatches 124; Indels 7; Gaps 4

QY 72 VRQLLTIEFMKDPEQEFMQAVREAVASIQPVFEKRPBLIP--IFKQIVEPERVITFRVS 129
Db 8 VDNFIARLKQRDPGQPEFHQAEEVYLRITLMPLEANPHYLQSIGILREMYEPEBAVLFRRVS 67

QY 130 WLDPDAGNIAQVRGFRVQYSSAIGPRYKGGARFRHPSVNLSTMKELAPEQIKNSLTITLPMG 189
Db 68 WDDDGKQVQVNRGYNRIQSSSAIGPRYKGGARFRHPSVNLSTMKELAPEQIKNSLTITLPMG 127

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ID Q9HVJ7 PRELIMINARY; PRT; 445 AA.
AC Q9HVJ7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DB Glutamate dehydrogenase.
GN Name-gdh; OrderedLocustNames=PA4588;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxId=287;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAOI;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Stover C.X., Plam X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Laibig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Iori S., Olson M.V.;
RA "Complete genome sequence of Pseudomonas aeruginosa PAOI, an
RT opportunistic pathogen."
RL Nature 406:959-964(2000).
DR EMBL:AE004872; MAG07976.1; -.
DR PIR; H83072; H83072.
DR HSSP; P24295; 1AUP.
DR GO; GO:0016491; P:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV_dehydrog_.
DR InterPro; IPR006096; GLFV_dehydrog_.
DR InterPro; IPR006097; GLFV_dehydrog_C.
DR Pfam; PF02028; GLFV_dehydrog_N.
DR Pfam; PF02812; GLFV_dehydrog_1.
DR PRINTS; PR00082; GLFVDRGNASE.
DR PROSITE; PS00074; GLFV_DEHYDROGNASE; 1.
KW Complete proteome.
SQ
SEQUENCE 445 AA; 48856 MW; 643BH12BC84F3418 CRC64;

Query Match 49.6%; Score 1309; DB 2; Length 445;
Best Local Similarity 59.2%; Pred. No. 2.2e-80;
Matches 263; Conservative 55; Mismatches 120; Indels 6; Gaps 4;

QY 72 VRQLTEIFMKDPEQGEFMAQVAREVAVSLQVFEKRPPELL--IFKQIVPERVITFRV 129
DB 5 VFAFLERLKRDPDQEFHQAVESVLRSLMPFLKAPHYLLEGIIRIVPERAILFRVP 64
QY 130 WDDAGNLQVNGFRVQYSSAIGPYKGLRPHPSVULSIMKFLAFQIFRNSLTLLPMG 189
DB 65 WDDQGRVAVNRGYVQMSAIGPYAGGRFHPSPVGLVLFKFLAFQVFRNSLTLLPMG 124
QY 190 GKGGSDFDPKGSDAEVMRFCSFMTLQRIHSYQDVDPAGDIGVAREIGVLFQGYKR 249
DB 125 GKGGSDFDPKGSDAEVMRFCSFMSLIRHVGADIDVPAGDIGVAREIGVLFQGYKR 184
QY 250 TKNYTGVLTPKQGEYGSSEIRPEATGYAVLFEVENVLKDKGSLKGRCLVSGAGNVAQ 309
DB 185 SNOFTSVLTGKGLSYGSLIRPEATGFGCVYFAQEWLXDRGRGFPDQGVVAISGSGNVAQ 244
QY 310 CAELLLEKGAIVLSLSDSGGYVYEPNGFTRQQLQAVQDMKKKNSARISYSKDTAVY 369
DB 245 AARKVEMGKXYSLSDSSEGTLYAEAGLSDEQWEYLMELKNVR--GRIREMEQFSLQL 303
QY 370 DRRKPEWELDQVYDIAPFCATONEIDHDAELLIKHCQYVVEGANNPSTNEAIHKKNK 429
DB 304 EGRRPGLC--DIAPFCATONEIDHDAELRIKLANGCVCVARGANPSTNEAVDLFLEAG 361
QY 430 IYCPKANAAGVAVSGLEMTQNRMSLMTREEVYDKLERIMKDIYDGA--MGPSPRYAV 488
DB 362 IYAPKANAAGVAVSGLEMTQNRMSLMTREEVYDKLERIMKDIYDGA--MGPSPRYAV 421
QY 489 DLAAGNINIGFTVADAVTAQAGAV 512
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DB 422 NYVKGANIGAFVADAMLAQGV 445

RESULT 8
Q9YJ71 PRELIMINARY; PRT; 444 AA.
AC Q9YJ71;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DB Glutamate dehydrogenase, NADP-specific.
GN OrderedLocustNames=NM1710;
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxId=491;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
RA Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
RA Dodson R.J., Nelson W.C., Gilm M.U., Deboy R.T., Peterson J.D.,
RA Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,
RA Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,
RA Clifton H., Clark E.B., Cotton M.D., Ueberback T.R., Khouri H.M.,
RA Qin H., Vamathevan J.J., Gill J., Scarlato V., Maignani V., Pizzo M.,
RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappaport R.,
RA Venter J.C.;
RA "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58."
RL Science 287:1809-1815(2000).
DR EMBL; AE002521; AAFA2057.1; -.
DR PIR; H81050; H81050.
DR HSSP; P24295; 1AUP.
DR TIGR; NM1710; -.
DR GO; GO:0016491; P:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV_dehydrog_.
DR InterPro; IPR006096; GLFV_dehydrog_.
DR InterPro; IPR006097; GLFV_dehydrog_C.
DR Pfam; PF02028; GLFV_dehydrog_N.
DR Pfam; PF02812; GLFV_dehydrog_1.
DR PRINTS; PR00082; GLFVDRGNASE.
DR PROSITE; PS00074; GLFV_DEHYDROGNASE; 1.
KW Complete proteome.
SQ
SEQUENCE 444 AA; 48490 MW; 8B2CFCCA89BE7DAF CRC64;

Query Match 49.3%; Score 1300.5; DB 2; Length 444;
Best Local Similarity 57.4%; Pred. No. 8.3e-80;
Matches 257; Conservative 72; Mismatches 104; Indels 15; Gaps 6;

QY 71 DVROLTEIFMKDPEQGEFMAQVAREVAVSLQVFEKRPPELL--PIFKQIVPERVITFRV 128
DB 3 DLAFTFANLKQHNPNQEPHQAVESVLRSLMPFLKAPHYLLEGIIRIVPERAILFRVP 62
QY 129 SMLDAGNLQVNGFRVQYSSAIGPYKGLRPHPSVULSIMKFLAFQIFRNSLTLLPMG 188
DB 63 TWDDKQGVQVNRGRVQMSAIGPYKGLRPHPSVULSIMKFLAFQIFRNSLTLLPMG 122
QY 189 GKGGSDFDPKGSDAEVMRFCSFMTLQRIHSYQDVDPAGDIGVAREIGVLFQGYKR 248
DB 123 GKGGSDFDPKGSDAEVMRFCSFMSLIRHVGADIDVPAGDIGVAREIGVLFQGYKR 182
QY 249 ITKNYTGVLTPKQGEYGSSEIRPEATGYAVLFEVENVLKDKGSLKGRCLVSGAGNVAQ 308
DB 183 IRNFSYVLTGKGLSYGSLIRPEATGFGCVYFAQAMLQTRNDSPEGRKVLISGSGNVAQ 242
QY 309 YAEELLLEKGAIVLSLSDSGGYVYEPNGFTRQQLQAVQDMKKKNSARISYSKDTAVY 367
DB 243 YAEARAQLQGAIVLSLSDSGNGVFLPSPDGKTEAQALAILKLVARE--RVATYAEQGIQ 301
QY 368 VDRRKPEWELDQVYDIAPFCATONEIDHDAELLIKHCQYVVEGANNPSTNEAIHKKNK 427
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Query Match      94.4%; Score 2489; DB 1; Length 523;
Best Local Similarity 96.8%; Pred. No. 3e-160;
Matches 486; Conservative 3; Mismatches 11; Indels 2; Gaps 1;

QY 11 VACAWRSARKDRAKAVASLEBQISAMDTTGDFTALOKAVKOMATKAGTEGIVHGIKMP 70
DB 24 VACARBSAKRDVAAR--RLRSRSPMDATTDFTLQAVKOMATKAGTEGIVHGIKMP 81

QY 71 DVROQLLTFEIMKDPBEOQEFMOAVREVAVSLQPVFEKRPELLPIFKQIVPERVITFRVSM 130
DB 82 ELRQLLTFEIMKDPBEOQEFMOAVREVAVSLQPVFEKRPELLPIFKQIVPERVITFRVSM 141

QY 131 LDDAGMLQVNRGRVYSSAIGPYKGLRPHSPVNSIMKFLAFEOIFKNSLTTLTLMGGG 190
DB 142 LDDAGMLQVNRGRVYSSAIGPYKGLRPHSPVNSIMKFLAFEOIFKNSLTTLTLMGGG 201

QY 191 KGSDDPDKGKSDAEVWRFQOSFMTLORHISVYQDVPAGDIGVGAREIGYLFQYKRTT 250
DB 202 KGSDDPDKGKSDAEVWRFQOSFMTLORHISVYQDVPAGDIGVGAREIGYLFQYKRTT 261

QY 251 KNYTVGLTPKGOEYGSSEIRPEATGYGAVLFVENVLKDGESLKGKRCIVSGAGVAYQYC 310
DB 262 KNYTVGLTPKGOEYGSSEIRPEATGYGAVLFVENVLKDGESLKGKRCIVSGAGVAYQYC 321

QY 311 ABELLEKGAIVLSLSSQGYVPEPNFTREQLQAVODMKKNNASISEKSTAYVGD 370
DB 322 ABELLEKGAIVLSLSSQGYVPEPNFTREQLQAVODMKKNNASISEKSTAYVGD 381

QY 371 RRRKPELDCQVDIAFPQATONEIDEHDAELLIKHGQYVVEGANMSTBEAIHKYKAGI 430
DB 382 RRRKPELDCQVDIAFPQATONEIDEHDAELLIKHGQYVVEGANMSTBEAIHKYKAGI 441

QY 431 IYCPGKANAAGVAVSGLEMTQNRMSLNTREBVRDLERIMKDIYDSAMGSPRRYVVDL 490
DB 442 IYCPGKANAAGVAVSGLEMTQNRMSLNTREBVRDLERIMKDIYDSAMGSPRRYVVDL 501

QY 491 AAGANTAGFTKVADAVKAGAV 512
DB 502 AAGANTAGFTKVADAVKAGAV 523

RESULT 2
Q81LF7 PRELIMINARY; PRT; 510 AA.
AC Q81LF7;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Glutamate dehydrogenase, putative.
GN ORFNames=PF14_0286;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
RA Gardner M.U., Hall N., Pung B., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyse S.,
RA Chan M.S., Nene V., Shalimov S.J., Suh B., Peterson J., Angiuoli S.,
RA Martin D.M., Fairlamb A.H., Fraunholz M.U., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrett B.;
RT "Genome sequence of the human malaria parasite Plasmodium
falciparum.";
RL Nature 419:498-511(2002).
EMBL: AE014820; AAN36899.1; -.
DR HSSP: P24295; IAUJ.
DR GO: GO:0016491; F:oxidoreductase activity; IEA.
DR GO: GO:0006520; P:amino acid metabolism; IEA.
DR InterPro: IPR006095; GLFV_dehydrog.

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DR InterPro: IPR006096; GLFV_dehydrog_C.
DR InterPro: IPR006097; GLFV_dehydrog_N.
DR Pfam: PF02028; GLFV_dehydrog_1.
DR Pfam: PF02812; GLFV_dehydrog_N_1.
DR PRINTS: PR00082; GLFVHDRGNASE.
DR PROSITE: PS00074; GLFV_DEHYDROGENASE_1.
SQ SEQUENCE 510 AA; 57343 MW; AC4000455297AC64F CRC64;

Query Match      52.1%; Score 1375; DB 2; Length 510;
Best Local Similarity 60.0%; Pred. No. 8.9e-85;
Matches 267; Conservative 66; Mismatches 104; Indels 8; Gaps 5;

QY 72 VQQLTFEIMKDPBEOQEFMOAVREVAVSLQPVFEKRPELLPIFKQIVPERVITFRVSM 131
DB 70 IELERKVSNNKNNPEFLQAEVTLSCLPFKDNVYIGLENIAPERVIOFRVPI 129

QY 132 DDAGMLQVNRGRVYSSAIGPYKGLRPHSPVNSIMKFLAFEOIFKNSLTTLTLMGGG 191
DB 130 NDKGHHKNNRGRVYSSAIGPYKGLRPHSPVNSIMKFLAFEOIFKNSLTTLTLMGGG 189

QY 192 GGSDDPDKGKSDAEVWRFQOSFMTLORHISVYQDVPAGDIGVGAREIGYLFQYKRTT 251
DB 190 GGSDDPDKGKSDAEVWRFQOSFMTLORHISVYQDVPAGDIGVGAREIGYLFQYKRTT 249

QY 251 KNYTVGLTPKGOEYGSSEIRPEATGYGAVLFVENVLKDGESLKGKRCIVSGAGVAYQYC 311
DB 250 SPEGLVLTGKNSIKWGSNTRAEATGYGAVLFVENVLKDNLENKRCIVSGAGVAYQYC 309

QY 312 EELLEKGAIVLSLSSQGYVPEPNFTREQLQAVODMKKNNASISEKSTAYVGD 369
DB 310 EELLEKGAIVLSLSSQGYVPEPNFTREQLQAVODMKKNNASISEKSTAYVGD 367

QY 370 DRRKPELDCQVDIAFPQATONEIDEHDAELLIKHGQYVVEGANMSTBEAIHKYKAG 429
DB 368 ENQKPEWNPIC--DIAFPQATONEINENDADLEITQKKCKIVGANNPTTHIKALHKLQNN 425

QY 430 IYCPGKANAAGVAVSGLEMTQNRMSLNTREBVRDLERIMKDIYDSAMGSPRRY--N 487
DB 426 IYCPGKANAAGVAVSGLEMTQNRMSLNTREBVRDLERIMKDIYDSAMGSPRRY--N 485

QY 488 VDLAAGANTAGFTKVADAVKAGAV 512
DB 486 SDLVAGANTAGFTKVADAVKAGAV 510

RESULT 3
Q7RQ39 PRELIMINARY; PRT; 1203 AA.
AC Q7RQ39;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Glutamate dehydrogenase.
GN Name=PY01264;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Koo J.T.W., Petrea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shalom S.J., van Aken S.B., Riedmiller S.B., Feldblum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabdi A., Cummings L.M.,
RA Florens L., Vates F.R., III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaideya A.B.,
RA van Lin L.H., Janse C.U., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";

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